REMARKS/ARGUMENTS

Status of the claims

With entry of the instant amendment, claims 10, 16, and 17 have been amended and claims 13, 15, 18, and 20-28 have been cancelled. Cancellation of subject matter is without prejudice to subsequent revival for prosecution in a continuation or divisional filing.

The amendments to the claims add no new matter.

Claims 10-12, 14, and 16, 17, 19, and 20 are under examination.

Sequence listing

Applicants have provided a substitute sequence listing. The amendments to the specification add no new matter. The format for the sequence listing of the nucleic acid entered as SEQ ID NO:9 and the polypeptide entered as SEQ ID NO:10 has been corrected. The "FEATURE" for SEQ ID NO:9 found on page 66 of the original Sequence Listing submitted on April 16, 2004, and on page 21 of the Substitute Sequence Listing submitted on October 15, 2004, respectively, included the "/note= "N signifies gap in sequence". Similarly, the "FEATURE" for SEQ ID NO:10 found on page 67 and page 22, respectively, included the "/note= "Xaa signifies gap in sequence". As such, the inclusion of a "gap" in these sequences does not conform to 37 C.F.R. § 1.822(e) which states that "A sequence with a gap or gaps shall be presented as a plurality of separate sequences, with separate sequence identifiers...". For this reason, the nucleic acid originally presented as SEQ ID NO:9 has been assigned SEQ ID NOS:9, 15 and 16, and the polypeptide originally presented as SEQ ID NO:10 has been assigned SEQ ID NOS:10, 17 and 18. This change is reflected in the amendments to paragraphs beginning on pages 4, 13, 14 and 19, where the additional respective SEQ ID NOS: have been inserted.

Amendments to Tables beginning on pages 15, 17 and 18 were made to correct typographical errors. The Table beginning on page 15 has been renumbered from "Table 5" to "Table 6", as there is already a "Table 5" beginning on page 11. Similarly, on page 17, "Table 6" and "Table 7" have been amended to "Table 7" and "Table 8", respectively, and on page 18, "Table 8" has been renumbered as "Table 9".

This amendment is accompanied by a floppy disk containing the above named sequences, SEQ ID NOS:1-92, in computer readable form, and a paper copy of the sequence information which has been printed from the floppy disk.

The information contained in the computer readable disk was prepared through the use of the software program "PatentIn" and is identical to that of the paper copy.

Claim objection

The objection to claim 17 has been addressed by the amendment to remove the period that inadvertently was included in the middle of the claim.

Rejection under 35 U.S.C. § 101, utility

Claims 10-19 are rejected as allegedly lacking utility. The Examiner alleges that there is no immediately obvious patentable use for Robo 1 antibodies, because, according to the Examiner, the specification fails to describe a biological function of human Robo 1. The Examiner contends that that the function of Robo-1 in axon growth that is disclosed in the specification is based only on homology and as such, is not credible. Applicants respectfully traverse this rejection.

First, the specification does in fact provide support for a biological function for Robo in the regulation of nerve cell function and morphology (page 3, line 4). The specification describes a new family of neuronal guidance receptors, robo proteins, and characterizes *robo* across various species including droposphila, *C. elegans*,, human, and mouse. The specification teaches that antibodies can be used, *e.g.*, in applications where pathology relates to improper or undesirable axon outgrowth, orientation or inhibition thereof (*e.g.*, page 13, lines 10-19). and that Robo inhibitors can be used to promote nerve cell growth (*e.g.*, page 3, line 10, first full paragraph). The specification also provides experimental evidence that robo is involved in axon growth. For example, the examples provide experiments showing that robo is expressed on longitudinally-projecting growth cones and axons (page 29, lines 12-17 of the first complete paragraph). The application additionally provides evidence that *robo1* is involved in mammalian nerve cell growth. The application demonstrates that rat *robo1* RNA is expressed in the rat

embryonic spinal cord (see, e.g., the last paragraph on page 31 bridging to page 32. This indicates that it encodes the function equivalent of Drosophila Robo1 (page 32, lines 11-13).

Robo compositions, e.g., robo-specific binding agents such as antibodies, therefore have a utility for diagnostic and therapeutic applications involving nerve growth. In addition, Robo antibodies have a readily apparent use in a laboratory setting, explained in detail below. These utilities meet the standards set forth in the MPEP at § 2107: they are credible, substantial, and specific.

Guidelines For Utility--MPEP § 21207

A. An Asserted Utility Must be Specific and Substantial

"[A] disclosure that identifies a particular biological activity of a compound and explains how that activity can be utilized in a particular therapeutic application of the compound does contain an assertion of specific and substantial utility for the invention." (MPEP § 2107.02.II.A)

The robo-related compositions have utility for the treatment of diseases or conditions related to abnormal axon orientation or growth

As indicated above, assertions of utility are present in the specification. Exemplary passages are also detailed below. Briefly, the specification teaches that Robo is involved in axon guidance, e.g., midline crossing (e.g., last paragraph of page 2, bridging to page 3) and that Robo polypeptides and antibodies can be used to modulate neuronal cell growth. For example, the inventors teach that Robo-specific binding agents can be used for pharmaceutical development and diagnostic and therapeutic purposes, e.g., to promote nerve cell growth (page 3, lines 9-15; page 4, lines 13-16) and/or for the treatment of pathology, wound repair incompetency or prognosis that is associated with improper or undesirable axon outgrowth, orientation or inhibition thereof (e.g., page 13, lines 10-19).

The application therefore identifies a particular biological activity of a Robo compound and explains how that activity can be utilized, e.g., in a pathological condition involving neuronal cell growth. Accordingly, the biological utility is a specific and substantial utility as set forth in the MPEP.

B. An Asserted Utility Creates a Presumption of Utility

"If the asserted utility is credible (i.e., believable based on the record or the nature of the invention), a rejection based on "lack of utility" is not appropriate." (MPEP § 2107.02.III.B)

"[T]o overcome the presumption of truth that an assertion of utility by the applicants enjoys,

Office personnel must establish that it is more likely than not that one of ordinary skill in the art
would doubt (i.e., "question") the truth of the statement of utility." (MPEP § 2107.02.III.B)

There is no evidence that one of skill would doubt the asserted utility

The biological utility is also credible. The Patent Office must treat as true a statement of fact made by an applicant in relation to an asserted utility, unless countervailing evidence can be provided that shows that one or ordinary skill in the art would have a legitimate basis to doubt the credibility of such a statement. The rejection appears to assert that the utility is not believable, because, according to the Examiner, the asserted utility is only based on homology among the Robo family members. However, as noted above, the specification in fact provides experimental evidence supporting the asserted utility. Furthermore, provided herewith is additional evidence to support the contention that one of skill would believe that the roborelated compositions are useful for identifying modulators that can be used in disease or conditions involving axon growth. Appendices A-D provide exemplary gene expression data showing that robo is expressed in adult tissues and is associated with conditions or diseases involving neuronal growth.

Marillat et al., J. Comp Neur. 442:130-155, 2002 (Appendix A) provides evidence that robo is also expressed in adult mammalian tissues. Marillat describes robo expression in the rat central nervous system from embryonic stages to adult age. The abstract of Marillat et al., teaches that slit (a robo ligand) and robo expression are upregulated postnatally. Page 152, second column, first full paragraph further teaches that the maintained high level expression of slit proteins and their receptors, i.e., robo proteins, in adult neurons suggest that the function of

the robo and slit proteins is not restricted to the control of axonal pathfinding and neuronal migration, but they are involved in synaptic plasticity.

Robo is also expressed in the human adult central nervous system. Appendix B provides data from the online database expression source Gene Normal Tissue Expression (GeneNote, http://bioinfo2.weizmann.ac.il/cgi-bin/genenote/home_page.pl). These data are from 1) hybridization studies using an array to obtain expression profiles of polyA+ RNA from twelve normal human tissues and 2) electronic Northern analysis. The array data and electronic northern are generated as described in the GeneNote methodology section, also provided in Appendix B. In brief, the data in the electronic northern is based on the origin and number of ESTs in Genbank that represent a locus. The data are derived from the Unigene dataset, which was mined for information about the number of unique clones per gene. Both the array analysis and electronic expression analysis show that robo is expressed in normal adult nervous tissue.

Further, enclosed is a paper showing the robo is expressed in injured central nervous system and spinal cord (Wehrle, et al., Eur J Neurosci. 22:2134-44, 2005, Appendix C, see, e.g, the abstract).

In summary, the supplemental material provided in Appendices A-D provide additional evidence supporting Applicants' assertion that robo proteins, including robo 1, play a role in the biological process of axon guidance and axon outgrowth, and that the claimed compositions have diagnostic and therapeutic utilities, *e.g.*, use for identifying modulators of robo function, which modulators can be used for treating conditions relating to abnormalities of axon growth. "If the record as a whole would make it more likely than not that the asserted utility for the claimed invention would be considered credible by a person of ordinary skill in the art, the Office cannot maintain the rejection" (MPEP §2107.02.VI). Thus, in order to apply a utility rejection to the instant claims, the Examiner must provide additional evidence that one of skill, in considering the totality of the evidence, would not be likely to believe the asserted utility. In the absence of such evidence, the asserted utility meets the requirements for credibility.

C. Many Research Tools Have a Clear, Specific, and Unquestionable Utility

"Some confusion can results when one attempts to label certain types of inventions as not being capable of having a specific and substantial utility based on the setting in which the invention is to be used. One example is inventions to be used in a research or laboratory setting. Many research tools... have a clear, specific and unquestionable utility.... An assessment that focuses on whether an invention is useful only in a research setting...does not address whether the invention is in fact "useful" in a patent sense." (MPEP § 2107.01)

The claimed subject matter has specific and substantial utility in a laboratory setting

Robo proteins, robo binding agents, and modulators of robo also have utility in a laboratory setting as a research tool for studies involving neuron growth. As indicated above, the MPEP explicitly cautions against labeling inventions as lacking specific and substantial utility based on the setting, such as a laboratory, in which the invention is to be used. In the case of robo and its associated compositions, utility in a laboratory setting is both specific and substantial.

A utility is specific if it is not applicable to a broad category in general (MPEP § 2107.01.I). As noted above, robo proteins play a role in axon guidance, for example, they are important in controlling midline crossing. This function is not applicable to a broad category, *i.e.*, proteins, in general. Common sense dictates that one of skill in the art employing robo antibodies (or other robo-related reagents) in a laboratory is in fact likely using robo compositions because of the role of robo in axon outgrowth and guidance, not simply non-specific reagents. Accordingly, in light of the guidelines provided in the MPEP, the utility is specific to the subject matter claimed.

The use of robo proteins and related compositions in a laboratory setting is also a substantial utility. The MPEP (§2107) defines a substantial utility as a real world use. Robo proteins and related compositions, e.g., antibodies, have a practical use, real-world use. For example, antibodies to robo proteins are offered for sale by Santa Cruz Biotechnology, Inc. s (see, Appendix D, a printout of available antibodies to various robo proteins). Although this is of course a post-filing listing of the antibodies, such antibodies must have a real-world use, or

there would be no market for them. Even though this market exists within the context of research, rather than diagnostics or therapeutics, this does not negate the utility of the claimed subject matter. A simple search of the literature shows that axon guidance is an active area of investigation, and hence, provides a practical and specific context for using robo antibodies in a laboratory setting..

Last, this is a credible utility. In order to find to the contrary, the Office personnel would have to establish that it would be more likely than not that one of ordinary skill in the art would doubt the truth of the utility. (MPEP § 2107.02.III.A). The rejection does not provide evidence that an ordinary artisan would believe that this utility is not real.

In view of the foregoing, the invention meets the requirements for utility. Applicants therefore respectfully request withdrawal of the rejection.

Rejection under 35 U.S.C. § 112, first paragraph written description

Claims 10-12, 14, 15, 18, and 19 are rejected as allegedly lacking written descriptive support. In particular, the Examiner alleges that the specification does not properly describe an antibody that binds to a polypeptide that has at least 95% identity to SEQ ID NO:8. Although Applicants disagree, in the interests of expediting prosecution, claim 10 has been amended to recite that the antibody specifically binds to SEQ ID NO:8.

In view of the foregoing, Applicants respectfully request withdrawal of the rejection.

Rejections under 35 U.S.C. § 112, second paragraph

Claims 10-19 are rejected as allegedly indefinite over the recitation of "Robo" in the terms "Rob-specific" and "Robo-mediated signaling" in claims 10 and 18, respectively. Although Applicants disagree, as the claims recite specific structural features that allow one of skill to determine the metes and bounds of the inventions, in the interests of expediting prosecution, the claims have been amended to delete the term "Robo". Applicants therefore respectfully request withdrawal of the rejection.

Rejection under 35 U.S.C. § 102(e)

Claims 10-19 are rejected as allegedly anticipated by McCarthy et al. in U.S. Patent Publication No. 2002/0150988. The Examiner contends that McCarthy discloses a polypeptide having 100% identity to the polypeptide 68-167 of SEQ ID NO:8. The sequence at issue in McCarthy, depicted in Figure 3, was first included in provisional application 60/062,017, filed October 10, 1997. Submitted herewith is a Rule 131 Declaration establishing that the invention was made in the United States prior to October 10, 1997, thus removing McCarthy et al. as prior art.

In Exhibit A to the attached Declaration, Applicants provide evidence that they obtained the sequence to human Robo-1 before October 10, 1997. Exhibit A, with dates redacted therefrom, is a printout of laboratory records showing the amino acid sequence of human Robo-1. The raw sequence file data were saved to an optical disk. The pages in Exhibit A show a computer analysis of sequence data comparing the human Robo-1 (H-Robo1 pep) sequence to those of other Robo proteins. The amino acid sequence was determined based on nucleic acid sequence. H-Robo1 pep includes the extracellular domain (five immunoglobulin domains and three fibronectin domains). Amino acids 68-167 of H-Robo1 pep are the first immunoglobulin domain and correspond to amino acids 68-167 of SEQ ID NO:8 in the application.

In view of the foregoing, it is respectfully submitted that the evidence provided in Exhibit A unequivocally establishes that the basic inventive concept of the claimed invention was conceived of and reduced to practice prior to October 10, 1997. Withdrawal of the rejection is respectfully requested.

Double patenting

This potential objection is most in view of the cancellation of claim 15.

Additional Species

In view of the foregoing, Applicants respectfully request that the Examiner extend examination to additional species.

CONCLUSION

Applicants believe all claims now pending in this Application are in condition for allowance. The issuance of a formal Notice of Allowance at an early date is respectfully requested.

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 415-576-0200.

Respectfully submitted,

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Appendix A

Spatiotemporal Expression Patterns of slit and robo Genes in the Rat Brain

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ABSTRACT

Diffusible chemorepellents play a major role in guiding developing axons toward their correct targets by preventing them from entering or steering them away from certain regions. Genetic studies in Drosophila revealed a repulsive guidance system that prevents inappropriate axons from crossing the central nervous system midline; this repulsive system is mediated by the secreted extracellular matrix protein Slit and its receptors Roundabout (Robo). Three distinct slit genes (slit1, slit2, and slit3) and three distinct robo genes (robo1, robo2, rig-1) have been cloned in mammals. However, to date, only Robo1 and Robo2 have been shown to be receptors for Slits. In rodents, Slits have been shown to function as chemorepellents for several classes of axons and migrating neurons. In addition, Slit can also stimulate the formation of axonal branches by some sensory axons. To identify Slit-responsive neurons and to help analyze Slit function, we have studied, by in situ hybridization, the expression pattern of slits and their receptors robo1 and robo2. in the rat central nervous system from embryonic stages to adult age. We found that their expression patterns are very dynamic: in most regions, slit and robo are expressed in a complementary pattern, and their expression is up-regulated postnatally. Our study confirms the potential role of these molecules in axonal pathfinding and neuronal migration. However, the persistence of robo and slit expression suggests that the couple slit/robo may also have an important function in the adult brain. J. Comp. Neurol. 442: 130-155, 2002. © 2002 Wiley-Liss, Inc.

Indexing terms: olfactory system; hippocampus; thalamus; cerebellum; axon guidance; migration

In the past decade, a large number of axon guidance molecules has been characterized (Tessier-Lavigne and Goodman, 1996). Remarkably, many of these novel molecules are diffusible, secreted by cells located at a distance from the growth cones they are acting on. The slit family is the most recently discovered family of chemotropic factors (Brose and Tessier-Lavigne, 2000). The first slit was identified in *Drosophila* embryo as a gene involved in the patterning of larval cuticle (Nusslein-Volhard et al., 1984). Subsequently, it was shown that Slit is synthesized in the central nervous system by midline glia cells and that, in its absence, longitudinal and commissural axons converge and coalesce abnormally at the midline (Rothberg et al., 1988, 1990; Sonnenfeld and Jacobs, 1994). More recent studies have shown that Slit is a chemorepulsive factor and a key regulator of midline crossing and axonal fasciculation (Battye et al., 1999; Rajagopalan et al., 2000a,b; Simpson et al., 2000a,b). Vertebrate homologues have since been found in virtually all taxa, from amphibians (Li

et al., 1999), fishes (Halloran et al., 2000; Yeo et al., 2001), birds (Vargesson et al., 2001), to rodents and humans (Holmes et al., 1998; Itoh et al., 1998; Brose et al., 1999; Yuan et al., 1999). In mammals, three slit genes (slit1-slit3) have been cloned. All slits encode large extracellular matrix proteins, composed from their N-terminus to their C-terminus of a long stretch of leucine-rich repeats, seven (in flies) to nine (in vertebrates) EGF repeats, flanking a domain named ALPS (Rothberg and Artavanis-Tsakonas,

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1992), LNS (Rudenko et al., 1999), or LG module (Hohenester et al., 1999). Human Slit2 and Drosophila Slit are cleaved in vitro and in vivo into two fragments, a 140-kDa N-terminal one and a 60-kDa C-terminal one (Brose et al., 1999; Kidd et al., 1999; Wang et al., 1999). These fragments have different biochemical characteristics. The C-terminal fragment is more diffusible than the larger N-terminal and full-length fragments, which are more tightly associated to the cell membrane (see below). In the vertebrate central nervous system (CNS) Slits have also been shown to be repulsive factors for developing axons projecting from the spinal cord (Brose et al., 1999), the olfactory bulb (Li et al., 1999; Nguyen-Ba-Charvet et al., 1999), the dentate gyrus (Nguyen-Ba-Charvet et al., 1999), the retina (Erskine et al., 2000; Niclou et al., 2000; Ringstedt et al., 2000), and the cortex (Shu and Richards, 2001). Interestingly, in rodents slit2 can stimulate axonal elongation and branch formation of sensory axons from the dorsal root ganglia (Wang et al., 1999). Moreover, in vivo and in vitro experiments suggest that Slit proteins control the migration of muscle precursors in fly embryos (Kidd et al., 1999; Kramer et al., 2001), of mesodermal cells in zebrafish embryos (Halloran et al., 2000; Yeo et al., 2001) and of several categories of tangentially migrating

accumbens nuclei

telencephalic interneurons in organotypic cultures (Hu, 1999; Wu et al., 1999; Zhu et al., 1999). Structure-function studies have shown that Slit's repulsive activities are associated with the leucine-rich repeats (Chen et al., 2001; Nguyen-Ba-Charvet et al., 2001a).

One major breakthrough toward the understanding of Slit function has been the recent discovery that the Roundabout (Robo) proteins are Slit receptors (Brose et al., 1999; Kidd et al., 1999; Li et al., 1999). The first robo gene, robo1, was identified in Drosophila with a comprehensive screen for genes controlling CNS midline crossing (Seeger et al., 1993). In robo1 mutants, ipsilateral axons that normally avoid the midline cross it and commissural axons cross and recross it repeatedly (Seeger et al., 1993). Robo is an evolutionary conserved family of transmembrane receptors (Zallen et al., 1998; Kidd et al., 1999; Rajagopalan et al., 2000b; Simpson et al., 2000b). They define a small subgroup within the immunoglobulin superfamily characterized by the presence of five immunoglobulin (Ig) -like domains followed by three fibronectin type III (FNIII) repeats, a transmembrane portion, and a long cytoplasmic tail containing robo-specific motifs (Kidd et al., 1998a; Rajagopalan et al., 2000b; Simpson et al., 2000b). To date, three robo genes have been found in flies

Abbreviations

Ac ·	accumbens nuclei	LRN	lateral reticular nucleus
AH	anterior hypothalamic nucleus	LS	lateral septum
AOB	accessory olfactory bulb	LSO	lateral superior olive
AON	anterior olfactory nucleus	m	mitral cell layer
AONe	anterior olfactory nucleus pars externalis	MA	medial nucleus of the amygdala
AONI	anterior olfactory nucleus pars lateralis	MAO	medial accessory olive
Aq	aqueduct	mes	mesencephalon
Ar	arcuate hypothalamic nucleus .	MG	medial geniculate nucleus
BM	basomedial nucleus of the amygdala	MGv	ventral medial geniculate nucleus
CA1	corni ammonii 1 field	mHb	medial habenula
CA3	corni ammonii 3 field	OB	olfactory bulb
CL	central lateral nucleus	oe	olfactory epithelium
CM	central median nucleus	PAG	periaqueductal gray
ChP	choroid plexus	Pavh	paraventricular hypothalamic nucleus
CPu	caudate putamen	Pe	periventricular hypothalamic area
Cu	cuneate nucleus	pn	pontine nucleus
DAO	dorsal accessory olive	PO	principal olive
DB ·	diagonal band of Broca	PV	paraventricular thalamic nucleus
DG.	dentate gyrus .	Rho	rhombencephalon
di	diencephalon	RMC	
dLG	dorsal lateral geniculate nucleus	RMS	red magnocellularis nucleus
Dmh	dorsomedial hypothalamic nucleus	Rt	rostral migratory stream
DN	deep cerebellar nuclei	Kt S	reticular nucleus
dTH	dorsal thalamus	SC	septum
egl	external granular layer		superior colliculus
ер	external plexiform layer	SN	substantia nigra
Et	epithalamus	Sth	subthalamic nucleus
fp	floor plate	svz	subventricular zone
g	glomerular layer	tel	telencephalon
GCL	granular cell layer .	Tu	olfactory tubercle
ge	ganglionic eminence	Tz	trapezoid body nucleus
Gr	gracile nucleus	vLG	ventral lateral geniculate nucleus
hil	hilus	VM	ventromedial thalamic nucleus
IC	inferior colliculus	VMH	ventromedial hypothalamic nucleus
ic	islands of Calleja	VNO	vomeronasal organ
ig IP	indusium griseum	VP	ventral pallidum
	interpeduncular nucleus	VPL	ventral posterior lateral nucleus
IO	inferior olive	VPM	ventral posterior medial nucleus
LA	lateral nucleus of the amygdala	V8	spinal trigeminal nucleus
LD	laterodorsal thalamic nucleus	VTA	ventral tegmental area
lge	lateral ganglionic eminence	√TH	ventral thalamus
LH	lateral hypothalamic nucleus	VZ	ventricular zone
lHb	lateral habenula	XII	hypoglossal nucleus
LL	lateral lemniscus	Zi	zona incerta
LP	lateroposterior thalamic nucleus	zli	zona limitans intrathalamica

(Kidd et al., 1998a; Rajagopalan et al., 2000a; Simpson et al., 2000b) and in mammals (Brose et al., 1999; Li et al., 1999; Yuan et al., 1999). In Drosophila, genetic and biochemical evidence indicates that Slit is a ligand of the robo1-robo3 receptors (Kidd et al., 1999; Rajagopalan et al., 2000b; Simpson et al., 2000b). Similarly, in vitro studies have shown that, in mammals, Slit1 (Yuan et al., 1999), Slit2 (Brose et al., 1999), and Slit3 (M.T.L. and A.C., unpublished data) bind with a similar affinity to Robo1 and Robo2 and that Slit binding is mediated in its N-terminal portion (Nguyen-Ba-Charvet et al., 2001a). However, it is not known whether Rig-1 (Yuan et al., 1999), the third vertebrate Robo-like protein, which lacks some cytoplasmic domains found in Robo1 and Robo2, is a receptor for Slit. It also remains to be determined whether in mammals Slit functions are mediated by Robos. Despite the importance of these molecules, the spatiotemporal expression of vertebrate robo and slit genes has only been partially reported, mostly at early embryonic stages (Holmes et al., 1998; Itoh et al., 1998; Brose et al., 1999; Liang et al., 1999; Nguyen-Ba-Charvet et al., 1999; Yuan et al., 1999; Erskine et al., 2000; Niclou et al., 2000; Ringstedt et al., 2000; Shu and Richards, 2001). In this study, we have performed an extensive in situ hybridization analysis of the expression patterns of slits and their receptors robo1 and robo2, in an attempt to identify neurons that could respond to Slits and also to gain further insights into Slit function in the developing and adult brain.

MATERIALS AND METHODS Animals

Wistar (IFFA-Credo, Lyon, France) and Sprague-Dawley rats (Janvier, Le Genest Saint Isle, France) were analyzed at different prenatal (embryonic day [E] 12, E15, E18, and E20) and postnatal ages (postnatal day [P]1, P3, P5, P10, and adult). The day of the vaginal plug was counted as embryonic day 0 (E0), and the day of birth as postnatal day 0 (P0). Pregnant dams were anesthetized with chloral hydrate (350 mg/kg). All animal procedures were conducted in strict compliance with approved institutional protocols.

E12–E15 embryos were fixed by immersion in 4% paraformaldehyde in 0.1 M phosphate buffer, pH 7.4 (PFA). Embryos from E20 and postnatal rats until P5 were perfused transcardially with 4% PFA. Whole embryos or brains were postfixed overnight in the same fixative, cryoprotected in 10% sucrose, frozen in isopentane (-55° C), and stored at -80° C until sectioning. P10 and adults were anesthetized and decapitated, and brains were immediately frozen in isopentane and stored at -80° C. Serial coronal, horizontal, and sagittal sections (25 µm) were cut with a cryostat and stored at -80° C before hybridization.

Cloning of rat Slit3 cDNA

Total RNAs from E15 brain were extracted with Trizol procedures (Invitrogen, Cergy-Pontoise, France). cDNAs were synthesized by using the first strand cDNA synthesis kit (Amersham, Orsay, France). cDNAs were used as template in a polymerase chain reaction (PCR) reaction. By using the following primers in PCR: primer 1, 5'-CTGGAGACCATGCACGGACGCATGTTC-3', and primer 2, 5'-AGTGGGCTCCTGCTGTACCACAATGCA-3', a single

1,749-bp fragment was yielded. This PCR product was identified by sequencing as a 1,749-bp partial rat slit3 sequence (nucleotides 1,777 to 3,426) and was cloned into pCR-II-topo vector (InVitrogen, Groningen, The Netherlands).

Riboprobes synthesis

cDNAs encoding rat slit1, slit2, robo1, and robo2 were described elsewhere (Brose et al., 1999). The in vitro transcription was carried out by using the Promega kit (Promega, Charbonnières, France) and probes were labeled either with digoxigenin-11-d-UTP (Roche Diagnostics, Meylan, France) or ³⁵S-UTP (>1,000 Ci/mM; Amersham).

In situ hybridization with digoxigeninlabeled riboprobes

Tissue sections from E12 to E20 embryos and postnatal rats until P5 were hybridized with digoxigenin-labeled riboprobes. Tissue sections were postfixed for 10 minutes in 4% PFA, washed in PBS (pH 7.4), treated with proteinase K (10 µg/ml; Invitrogen) for 7 minutes 30 seconds, postfixed for 5 minutes in 4% PFA, washed in PBS, acetylated, washed in PBS 1% Triton X-100. Slides were incubated 2 hours at room temperature with hybridization buffer (50% formamide, 5× SSC, 1× Denhardt's, 250 μg/ml yeast tRNA, and 500 μg/ml herring sperm DNA, pH 7.4). Then, tissue sections were hybridized overnight at 72°C with riboprobes (1/200). After hybridization, sections were rinsed for 2 hours in 2× SSC at 72°C, and blocked in 0.1 M Tris, pH 7.5, 0.15 M NaCl (B1) containing 10% normal goat serum (NGS) for 1 hour at room temperature. After blocking, slides were incubated overnight at room temperature with anti-DIG antibody conjugated with the alkaline phosphatase (1/5,000, Roche Diagnostics) in B1 containing 1% NGS. After washing in B1 buffer, the alkaline phosphatase activity was detected by using nitroblue tetrazolium chloride (337.5 µg/ml) and 5-bromo-4-chloro-3-indolyl phosphate (175 µg/ml) (Roche Diagnostics). Sections were mounted in Mowiol (Calbiochem/Merck, Carlstadt, Germany).

In situ hybridization with ³⁵S-labeled riboprobes

Tissue sections of P10 and adult brains were hybridized with 35S-labeled riboprobes. Sections were post-fixed 15 minutes in 4% PFA, washed in PBS, acetylated, washed in PBS, dehydrated in graded ethanols and air-dried. Sections were covered with hybridization buffer containing 5.10⁵ cpm/µl of riboprobes (50% formamide, 0.3 M NaCl, 20 mM Tris-HCl pH 7.4, 5 mM EDTA, 1× Denhardt's, 10% dextran sulfate, 10 mM DTT, 10 mM NaH₂PO₄, pH 8.0 and 250 µg/ml yeast tRNA, pH 7.4). Slides were hybridized overnight at 48°C in humid chamber. After hybridization, sections were rinsed for 30 minutes in $5 \times SSC$ at 48°C and for 20 minutes in 2.5× SCC at 60°C. Sections were then treated for 30 minutes with 20 mg/ml Rnase A at 37°C, washed in 2× SSC and in 0.1× SSC for 15 minutes each, dehydrated, and air-dried. Autoradiograms were obtained by apposing the sections to hyperfilms (βmax, Amersham) for 3 days. For histologic analyses, the slides were dipped in photographic emulsion (NTB2, Kodak) and exposed for approximately 12 days. Then, slides were developed at 14°C D19 (Kodak), fixed in AL4 (Ilford) and subsequently rinsed, dehydrated, and mounted with cytoseal 60 (Stephens Scientific, Riverdale,

TABLE 1. Spatiotemporal Distribution of robo1 (1) and robo2 (2) mRNA in the Telencephalon1

Telencephalon	. E15	E18	E20	P0	P 5	P10	Adult
Olfactory system							
Olfactory epithelium	- 2	- 2	nd	nd	nd	nd	- 2
Mitral cells	- 2	- 2	1 2	12	1 2	1 2	12
Anterior olfactory n.		12	1 2	1 2	1 2	1 2	1 2
Accessory olfactory bulb	- 2	- 2	- 2	- 2	1 2	1 2	12
Cortex							
Marginal zone	-2						
Cortical plate	1 –	12	1 2				
Intermediate zone	- 2	- 2	- 2				
Subventricular zone ²	- 2	1 2	12		12	1 2	1 2
II–III				- 2	1 2	12	1 2
IV							
Ÿ				12	1 2	1 2	1 2
VI		•		- 2	-2	12	12
Enthorinal		12	1 2	1 2	12	1 2	12
Piriform	- 2	- 2	- 2	- 2	12	1 2	12
Retrosplenial				1 -	1 -	1 -	1-
Induseum griseum		1-	1 –	ī -	i -	î -	i-
Tenia tecta		i-	ī -	ī -	i -	12	12
Hippocampal system		•	<u>-</u>	-	_		
CA1	1-	1-	12	12	12	1 2	12
CA3	ī -	1 –	1 2	1 2	12	1 2	. 12
Dentate gyrus				i -	12	12	12
Subiculum		- 2	- 2	- 2	- 2	-2	-2
Basal ganglia		_	· -	=	-		2
Caudate putamen	12	12	1 2	12	12	12	12
Accumbens n.	12	1 2	12	12	12	12	12
Globus pallidus (lateral)	12	1 2	12	12	12	1 2	12
Basal telencephalon							1.4
Septum							
Islands of Calleia		1-	1 -	1 -	1 -	1 -	1-
Olfactory tubercle	-2	ī 2	12	ī 2	12	i -	i-
· Amygdaloid complex		i-	1 2	12	12	12	12

E, embryonic day; P, postnatal day; n., nucleus; nd, not determined; -, not detected.

² From P0, we refer to the anterior subventricular zone.

NJ). For the determination of labeled structures, we mostly used the nomenclature of Paxinos et al. (1991), for embryos, and from Paxinos and Watson (1986) for postnatal ages. Images were captured with a Zeiss Axiophot microscope, scanned with Nikon Coolscan II, and processed with Photoshop 6.0 (Adobe).

RESULTS Olfactory system

slit's and robo's mRNAs were detected in every component of the olfactory system, but in most cases, each neuronal population expressed only one of the receptors or one of the ligands (Tables 1 and 2).

Main olfactory system. Olfactory neurons in the olfactory epithelium were found to express high levels of robo2 mRNAs, as early as E12-E13 (Fig. 1A,B), shortly after they have sent their first axons toward the olfactory bulb (Lopez-Mascaraque et al., 1996). This pattern of robo2 expression was maintained at E18 (Fig. 1E; Table 1) and in the adult olfactory epithelium (Fig. 1C; Table 1). slit1 mRNA was first detected in olfactory neurons from E18 (Fig. 1F; Table 2). The comparison of robo2 and slit1 expression pattern on adjacent sections showed that slit1 was only expressed in restricted zones of the olfactory epithelium, although we did not try to determine whether these correspond to known olfactory projection zones (Yoshihara et al., 1997). robo1, slit2, and slit3 transcripts were not detected in the olfactory epithelium at all embryonic stages (Fig. 1D; Table 1 and data not shown). However, at E18, slit2 was highly expressed in mesenchymal cells surrounding the olfactory epithelium (not shown). Olfactory axons are known to contain, mRNAs, and at P5, slit3 mRNAs could be found in olfactory axons ending in

the glomeruli, indicating that olfactory receptor neurons also expressed *slit3* at this stage (Fig. 2I).

In the olfactory bulb, robo1 expression was detected around birth in mitral cells (Fig. 2A; Table 1). In the adult, mitral cells still expressed high levels of robo1 mRNAs, but also periglomerular cells in the glomerular layer and some neurons in the external plexiform layer, corresponding probably to tufted cells (Fig. 2B). Similarly, mitral cells and most interneurons in the olfactory bulb expressed robo2 from E13 onward (Figs. 1E, 2C,D; Table 1). From P5, it became clear that robo2 transcripts were found in all OB neurons to the exception of periglomerular cells (compare Fig. 2C,D with 2B). From E15 to E18, only slit1 was found in the olfactory bulb, whereas slit2 and slit3 were not detected. During this period slit1 was expressed in subsets of mitral cells and in scattered cells around the granular cell layer (Fig. 1F; see also Nguyen-Ba-Charvet et al., 1999). It decreased at later stages and was not detected in the olfactory bulb of newborns (Fig. 2E). However, in the adult, slit1 was highly expressed in the granule cell layer, and at a lower level in mitral cells, periglomerular cells, and neurons of the external plexiform layer (Fig. 2F). slit2 was still absent from the OB at P5 (Fig. 2G; Table 2), but in the adult, it was weakly expressed in granule cells and periglomerular cells (Fig. 2H). slit3 expression appeared around birth, and at P5 slit3 was found in the mitral cells (Fig. 2I; Table 2). From P10, slit3 expression decreased and it was not detected in the adult olfactory bulb (Fig. 2J).

In organotypic cultures, Slit1 and Slit2 proteins can repel OB interneurons migrating through the rostral migratory stream (RMS) from the subventricular zone (SVZ) to the OB (Hu, 1999; Wu et al., 1999). Moreover, Robo ectodomain can block this repulsive effect. However, the

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TABLE 2. Spatiotemporal Distribution of slit1 (1), slit2 (2), and slit3 (3) mRNA in the Telencephalon1

Telencephalon	E15	E18	E20	P0	P 5	P10	Adult
Olfactory system							
Olfactory epithelium	1	1 – –	nd	nd	. nd	nd	nd
Mitral cells	1	1	3	3	3		
Anterior olfactory n.		3	- 23	-23	-23	123	1 2 3
Accessory olfactory bulb					1 – 3	1-3	1-3
Cortex							1-0
Marginal zone	3						
Cortical plate	1	1	12-				
Intermediate zone							
Subventricular zone ²					1	1	1
II-III					3	3	3
IV	•						
V				123	. 123	123	123
VI				1	1-3	1-3	1-3
Enthorinal	123	123	123	123	123	123	123
Piriform	3	1 – 3	1 - 3	1 - 3	123	123	123
Retrosplenial				1 - 3	1-3	1-3	1-3
Induseum griseum		1 – 3	1-3	1 – 3	1-3	1-3	1-3
Tenia tecta		1 – 3	1-3	1 - 3	1 - 3	1-3	1-3
Hippocampal system		•			- •	4-0	1-3
CA1	1 - 3	1 – 3	1-3	-23	-23	123	1-3
CA3	123	1 2 3	123	123	123	123	123
Dentate gyrus	-2-	-23	-23	-23	-23	123	123
Subiculum	1-	1 – 3	1-3	1-3	1-3	1-3	1-3
Basal ganglia	-		- •			1-0	1-3
Caudate putamen	1	1 – –	1		3	3	1-3
Accumbens n.					3	3	3
Globus pallidus (medial)					1	1	1
Basal telencephalon					<u>-</u>	•	
Septum	12-	12-	12-	12-	12-	12-	12-
Islands of Calleia							3
Olfactory tubercle				3	3	3	-23
Bed stria terminalis n.	1-3	1 – 3	1-3	1 - 3	1-3	1-3	1-3
Amygdaloid complex			~-3	123	123	123	123

E, embryonic day; P, postnatal day; n., nucleus; nd, not determined; -, not detected.
 From P0, we refer to the anterior subventricular zone.

expression of Robo in cells migrating in the RMS had never been determined. We found that in the adult, cells migrating in the RMS express high levels of robo2 and low levels of robo1 mRNAs (Fig. 2B,D and not shown). These migrating cells were also found to express very high levels of slit1 transcripts (Fig. 2F), which is difficult to reconcile with the actual model of Slit/Robo function in this system (see Discussion section).

Accessory olfactory system. At E18, we found that slit1 and robo2 were expressed in the vomeronasal organ (VNO). However, both genes were found in distinct layers: robo2 was detected in the basal part of the VNO, whereas slit1 was restricted to the apical part of the VNO (Fig. 1E,F). These neurons project to distinct domains in the accessory olfactory bulb (see Discussion section; Mori et al., 2000). slit2, slit3, and robo1 were not expressed in the embryonic VNO (Fig.1D and not shown). From E15 to birth, only robo2 was detected in the accessory olfactory bulb (AOB) the target of VNO axons (Table 1 and not shown). This expression pattern evolves rapidly after Po, such as by P5 robo1, robo2, slit1, and slit3 were all detected in the AOB (Fig. 2A,C,E,I; Tables 1 and 2). robo1, robo2, and slit3 were found in the mitral and external plexiform cell layers (Fig. 2A,C,I). At that stage, slit1 and slit3 were also present in the glomerular layer, most likely in VNO axons (Fig. 2E,I). Slit2 was not expressed in the AOB (Fig. 2G; Table 2).

Other olfactory structures. At E13-E15, cells migrating from the olfactory epithelium toward the forebrain strongly expressed robo2 mRNA (Figs. 1B, 3D). These cells are most likely neurons secreting luteinizing hormonereleasing hormone (LHRH), on their way from the olfactory epithelium to the septal preoptic nuclei and the hypothalamus (Schwanzel-Fukuda and Pfaff, 1989; Schwarting et al.,

2001). However, they might also be glial ensheathing cells of the olfactory nerve, which start migrating from the olfactory epithelium at that stage (De Carlos et al., 1995).

Mitral, middle, and deep tufted cells in the olfactory bulb, project ipsilaterally to the anterior olfactory nucleus (AON) and to higher olfactory centers, including the piriform cortex, the olfactory tubercle, and some amygdaloid nuclei, collectively referred to as the primary olfactory cortex (for a review see Shipley and Ennis, 1996). By E18, robo and slit genes were present in all these regions (Figs 2, 3; Tables 1 and 2).

The AON is a laminated structure that can be subdivided in different regions based on their connections and cytoarchitecture. Neurons from the AON send axons to other components of the olfactory cortex and to the contralateral OB, this projection constituting a large part (the anterior arm) of the anterior commissure. In the AON, robo1, robo2, and slit3 expression started at E18, whereas slit1 and slit2 expression started, respectively, at P10 and E20 (Tables 1 and 2). At P5, all genes to the exception of slit1 were detected in the AON (Fig. 2). robo1 and slit2 were found in the internal part of the AON, whereas robo2 and slit3 were both expressed in the external and internal part. This expression was unchanged in the adult except for slit1, which was up-regulated and became highly expressed in the AON.

In the piriform cortex, only robo2 was detected from E15 to adulthood (Fig. 3D-F), whereas robo1 was not detected (Fig. 3A-C). slit1 and slit2 were also expressed in some of these structures such as the amygdala (see below). The taenia tecta (Tables 1 and 2 and not shown), which projects to the OB, and the indusium griseum (a structure just dorsal to the corpus callosum and related to the hippocampus, see Figs. 4H, 5C,D; Tables 1 and 2), which

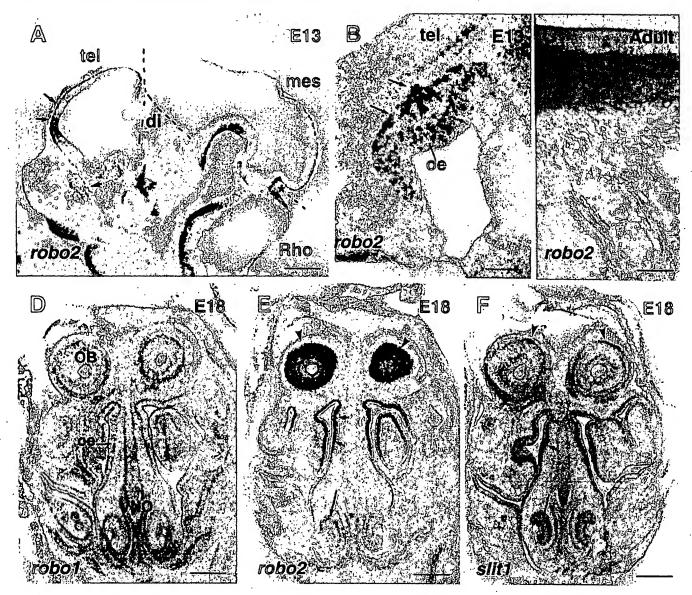


Fig. 1. robo1, robo2, and slit1 expression in the embryonic rat olfactory system. Sagittal (A) and coronal (B-F) sections were hybridized with digoxigenin-labeled riboprobes for robo1 (D), robo2 (A, B, C) and slit1 (F). A,B: At embryonic day (E) 13, robo2 is already detected in the telencephalon (tel), the alar and basal plates of the diencephalon (di) and the mesencephalon (mes). robo2 is also expressed in the cortical plate (arrows), in the cerebellar anlage (asterisk). In the olfactory epithelium (short arrow in A), robo2 is expressed in olfactory receptor neurons of the olfactory epithelium (oe) and in migrating cells (arrows in B) possibly LHRH neurons or glial ensheathing cells. C: In the adult, robo2 is still expressed in the olfactory receptor neurons of the olfactory epithelium (oe). D-F: At E18, robo1

(D) is not expressed in the olfactory system, whereas robo2 (E) is highly expressed in the mitral cell layer of the olfactory bulb (arrowheads) and in olfactory receptor neurons (short arrows). robo2 is also detected in the basal part of the vomeronasal epithelium (long arrow in E). In the olfactory bulb, slit1 (F) is present in a subset of mitral cells (arrowheads) and in scattered cells throughout the granular cell layer (asterisk). slit1 is also weakly expressed in olfactory receptor neurons (short arrows in F) and in the apical part of the vomeronasal epithelium (long arrow). OB, olfactory bulb; Rho, rhombencephalon; VNO, vomeronasal organ. Scale bars = 1 mm in A, 220 μ m in B, 31 μ m in C, 500 μ m in D-F.

receives direct projections from the olfactory bulb, both expressed from E18 to adult, robo1, slit1, and slit3 mR-NAs. At E15, the olfactory tubercle only expressed robo2 (Fig. 3D), then both robo1 and robo2 from E18 to P5 (Fig. 3B,E), and only robo1 from P10 to the adult (Fig. 3C). In contrast, no slits expression could be observed in this region before birth, when slit3 started to be detected (Table 2 and not shown). This expression of slit3 was main-

tained at a high level in the adult (Fig. 4I), and at this stage, neurons of the olfactory tubercle also expressed a low level of *slit2* (Fig. 4F).

Basal telencephalic structures

From E15 to the adult stage, we found that only robo1 is expressed in the Islands of Calleja (Fig. 3C; Table 1),

whereas both slit1 and slit3 were present in the basal stria terminalis (not shown, Table 2).

Septum. Olfactory bulb axons have also been shown to be repelled by a chemorepulsive factor released by the sep-

robo2

tum (Pini, 1993). Interestingly, we found that from E14, slit1 and slit2 were expressed in the septum with slit1 more highly and broadly distributed than slit2 (Fig. 4A,D; Table 2). In the adult, slit1 was expressed in the dorsal part of the lateral septum and the triangular nucleus. slit3 mRNA was never detected in the septum (Table 2). A low expression of robo1 and robo2 were also found in the septum at E14, but it was not detected at E18 (Fig. 3A,B).

Striatum. At E15, robo1 was expressed in the entire striatal anlage (Fig. 3A), whereas robo2 expression was restricted to a dorsal domain (Fig. 3D). From E18, robo1 and robo2 were expressed in postmitotic neurons of the caudate putamen and the nucleus accumbens (Fig. 3B,C,E,F; Table 1). At E15, slit1 was expressed in the striatal anlage at the level of the ventricular and subventricular zones of the ganglionic eminences (Fig. 4A). At E18, slit1 expression was still detected in the striatal SVZ (Fig. 4B). From birth, slit1 was restricted in the caudateputamen to scattered large neurons, probably cholinergic interneurons (Fig. 4C). slit2 was never detected in the striatum (Fig. 4D-F). slit3 expression appeared late in development from P5 (Table 2) in the lateral part of the caudate-putamen (Fig. 4G-I). From P0, slit1 was expressed in the medial globus pallidus (Table 2 and not shown), whereas robo1 and robo2 were expressed in the lateral globus pallidus (Table 1 and not shown).

Amygdala. slits and robos genes exhibited a distinctive pattern of expression in the developing amygdala. All slit genes were expressed from birth in the lateral and medial nuclei (Fig. 7G,H,J; Table 2 and not shown), which correspond, respectively, to the pallial and pallidal components of the amygdaloid complex (Puelles et al., 2000). On the contrary, robo1 was expressed at high levels only in the basomedial nucleus (Fig. 7E and not shown), whereas in this nucleus, robo2 exhibited a low level of expression (Fig.

Fig. 2. robos and slits expression in the postnatal rat olfactory bulb. Coronal sections were hybridized with digoxigenin-labeled riboprobes (A,C,E,G,I), or 35S-labeled riboprobes (B,D,F,H,J), for robo1 (A,B), robo2 (C,D), slit1 (E,F), slit2 (G,H), and slit3 (I,J). A: At postnatal day (P) 5, robo1 is highly expressed in the mitral cell layer of the accessory olfactory bulb (AOB) and in the lateral part of the accessory olfactory nuclei (AONI). In the olfactory bulb, robo1 is only found in the mitral cell layer (m). B: In the adult, robo1 is still expressed in the AON. In the olfactory bulb, robo1 is found in the mitral cell layer (m), in periglomerular cells of the glomerular layer (g), in neurons of the external plexiform layer (ep), and at a weak level in the granular cell layer (asterisk). robo1 is also detected in the subventricular zone (arrow). C: At P5, robo2 is highly expressed in the mitral cell layer of the AOB and in the lateral part (AONI) and the external part (AONe) of the accessory olfactory nuclei. In the olfactory bulb, robo2 is strongly expressed in mitral cells and in the external plexiform layer (arrows). D: In the adult, robo2 expression is maintained in the AON. in all olfactory bulb neurons except in periglomerular cells. robo2 is also highly expressed in the subventricular zone (arrow). E: At P5, slit1 expression is weak in olfactory glomeruli (arrows) and in the olfactory bulb and AOB, probably in axons from the olfactory epithelium and VNO. F: In the adult, slit1 is found in the AON, the subventricular zone (arrow), the granular cell layer and at a low level in mitral, external plexiform, and periglomerular cell layers. G: At P5, slit2 is only detected in the AONI. H: In the adult, slit2 is still expressed in the AON and is also detected at a low level in the granular cell layer. I: At P5, slit3 is expressed in mitral cells of the olfactory bulb, in the glomeruli (short arrows), in the mitral and glomerular layers of the AOB (long arrow), and in the AON1 and AONe. J: In the adult, slit3 expression is down-regulated except in the AON. Scale bars = 440 μ m in A,C,E,G,I, 750 μ m in B,D,F,H,J.

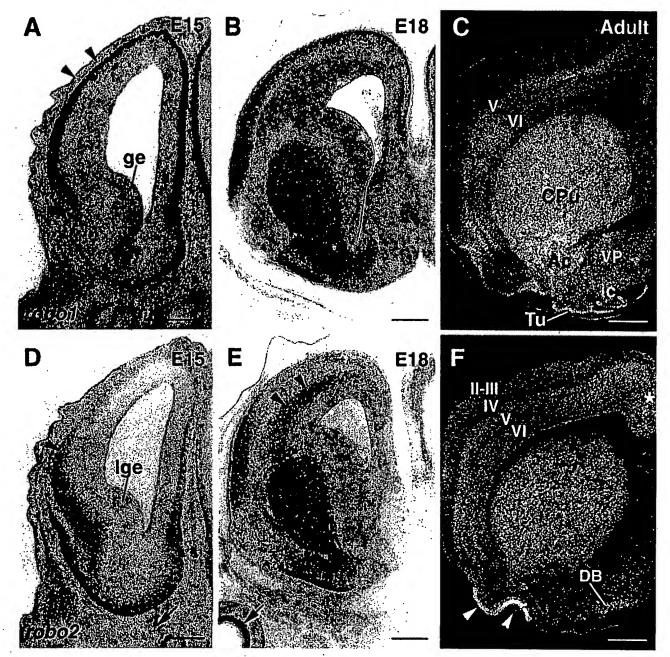


Fig. 3. Expression pattern of robos in the developing rostral telencephalon. Coronal sections were hybridized with digoxigenin-labeled riboprobes (A,B,D,E), or with ³⁵S-labeled riboprobes (C,F) for robo1 (A-C) and robo2 (D-F). A-C: At embryonic day (E) 15 (A), robo1 is highly expressed in the cortical plate (arrowheads) and in the ventricular zone of the ganglionic eminence (ge). From embryonic day (E) 18 (B) until adult (C), robo1 is expressed in the cortex, the caudate putamen (CPu), the accumbens nucleus (Ac), the olfactory tubercle (Tu), the islands of Calleja (ic), and the ventral pallidum (VP). In the adult cortex, robo1 is restricted to layers V-VI. D: At E15, robo2 expression is restricted to the cortical plate of the limbic cortex (ar-

rowhead), the lateral part of the ganglionic eminence (lge), the piriform cortex, and the olfactory tubercle. Likewise, robo2 is expressed in putative LHRH migrating neurons (arrow). E,F: From E18 (E) to adult (F), robo2 is highly expressed in the caudate putamen and the accumbens nucleus. At E18, robo2 is detected in the intermediate zone of the neocortex (arrowheads), and in the retinal ganglion cells (arrow in E). In the adult neocortex (F), robo2 is found in cortical layers II-III, Va, and VI, the piriform cortex (arrowheads), in the diagonal band of Broca (DB), and in the cingulate cortex (asterisk). Scale bars = 1,400 μm in A,D, 550 μm in B,E, 1,200 μm in C,F.

7B,F; Table 1; and not shown). This basomedial nucleus belongs to the striatal portion of the amygdaloid complex. In addition, *robo2* was also expressed in scattered neurons in the anterior amygdala area (not shown).

Cerebral cortex

All five genes were expressed in the cortex but often in different layers. *robo1* and *robo2* were first detected in the telencephalic vesicles from E13 (Fig. 1A, not shown, see

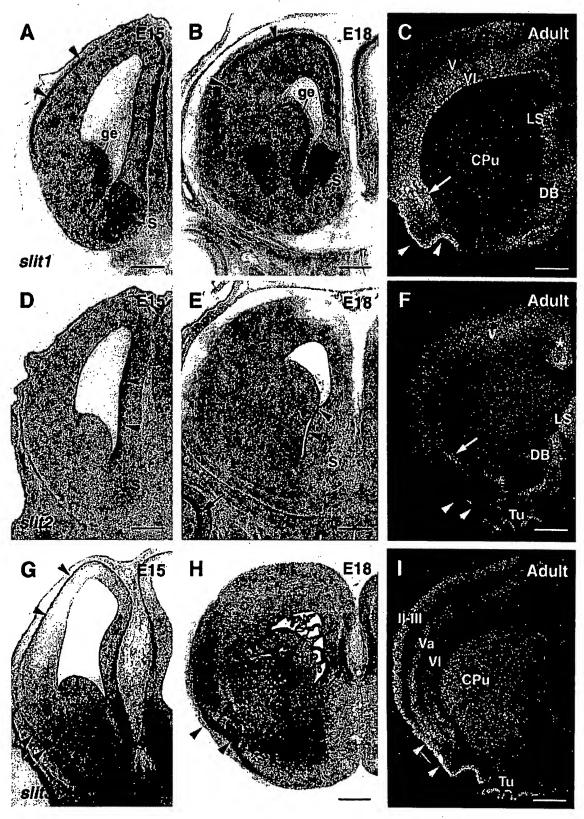


Fig. 4. Expression pattern of slits in the developing rostral telencephalon. Coronal sections were hybridized with digoxigenin-labeled riboprobes (A,B,D,E,G,H), or with 35 S-labeled riboprobes (C,F,I) for slit1 (A-C), slit2 (D-F), and slit3 (G-I). A-C: From embryonic day (E) 15 (A) to E18 (B), slit1 expression is restricted to the cortical plate of the cortex (arrowheads in A and B), the ventricular zone and subventricular zone of the ganglionic eminence (ge), and the septum (S). In the adult (C), slit1 is detected in cortical layer VI, the piriform cortex (arrowheads), and the claustrum (arrow). slit1 is also expressed in the lateral septum (LS), the diagonal band of Broca (DB), and some dispersed interneurons in the caudate putamen (CPu). D-F: From embryonic (B) (D) to E18 (E), slit2 is weakly detected in the ventricular zone (arrowheads) and in postmitotic neurons of the septum (S). At E18 (E), slit2 is also present in the retina (arrow). In the adult (F), slit2 is

detected in the layer V of the cortex and is at the highest level in the cingulate cortex (asterisk). It is also detected in cells of the lateral septum (LS) and in the diagonal band of Broca (DB). A weak expression of slit2 is also observed in the piriform cortex (arrowheads), the claustrum (arrow), and the olfactory tubercle (Tu). G-I: At E15 (G), slit3 is highly expressed in the superficial cortical plate of the cortex and in the piriform cortex (arrowheads). At E18 (H), slit3 expression decreased in the cortex but is maintained in the piriform cortex until adult (arrowheads in H and I). slit3 is also expressed in the indusium griseum (arrow in H). In the adult cortex, slit3 is highly detected in the layers II-III and Va. slit3 is also expressed in the caudate putamen (CPu) and in the olfactory tubercle (Tu). ChP, choroid plexus. Scale bars = 1,400 µm in A,D,G, 550 µm in B,E,H, 1,200 µm in C,F,I.

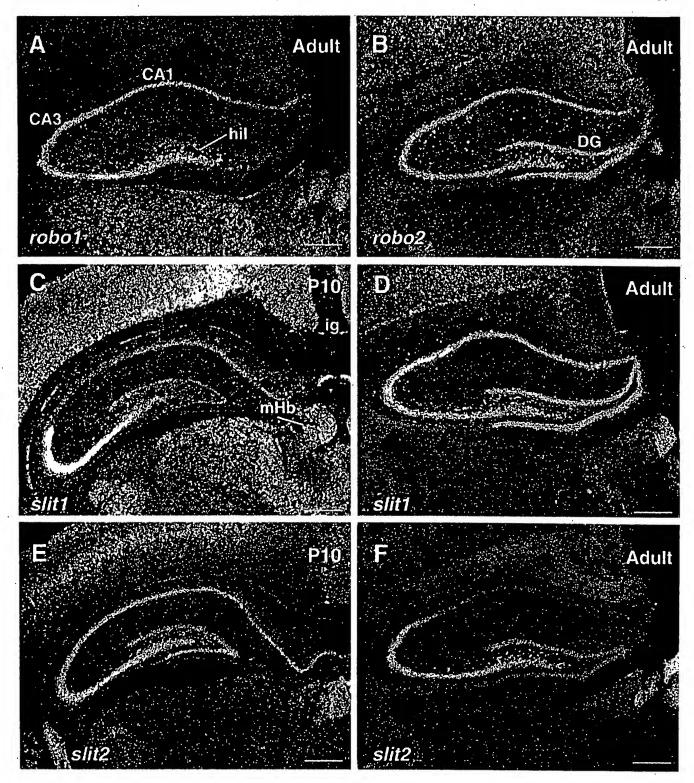


Fig. 5. robos and slits expression in the postnatal hippocampus. Coronal sections (A-F) were hybridized with ³⁵S-labeled riboprobes for robo1 (A), robo2 (B), slit1 (C,D), and slit2 (E,F). A,B: In the adult, a strong expression of robo1 was detected in the pyramidal cell layer of CA3 and in scattered neurons of the hilus (hil). A lower expression was detected in the pyramidal cell layer of CA1. robo2 (B) is strongly expressed in the pyramidal cell layer of CA1 and CA3 and in the granular cell layer of the dentate gyrus (DG). robo2 is also detected in scattered cells outside the pyramidal cell layer. C,D: At postnatal day

(P) 10 (C), slit1 labeling is intense in CA3 pyramidal neurons and weaker in CA1 pyramidal neurons and in the dentate gyrus, whereas in the adult (D), slit1 expression is up-regulated in CA1 pyramidal neurons and in the DG. E,F: At P10 (E), slit2 is highly expressed in the pyramidal neurons of CA1–CA3 subfields and in the granular cell layer of the DG, whereas in the adult (F) slit2 expression is downregulated in CA1 pyramidal neurons and in the DG. ig, indusium griseum; mHb, median habenula. Scale bars = 500 μm in A,B,D,F, 450 μm in C,E.

also Yuan et al., 1999). At E15, robo1 mRNA was expressed in the entire cortical plate (Fig. 3A), whereas robo2 was restricted to the cortical plate of the presumptive limbic cortex (Fig. 3D). By E18, the expression patterns of robo genes was unchanged in the cortical plate (Fig. 3B, E). robo1 remained in the superficial layers of the lateral, dorsal, and medial cortex, whereas robo2 was expressed in internal cortical layers and in the ventral pallium (claustrum and piriform cortex). In addition, robo2 was also found in the intermediate zone. The neocortical lamination is clearly settled by P5, and from this stage to the adult, robo2 was expressed at various levels in all cortical layers except in layer IV (Fig. 3F; Table 1). Interestingly, robo2 was strongly expressed in the remaining subplate neurons (layer VIb). robo1 expression became restricted to layers V and VI (Fig. 3C; Table 1), the most superficial neurons of neocortical layer II and pyramidal neurons of layer II in the retrosplenial and cingular cortices. slits were also all expressed in the cortex but each with a distinct spatiotemporal pattern. From E13, slit1 mRNA was expressed in the entire cortical plate, slit3 was only detected in the cortical and hippocampal marginal zone from E15 and slit2 was not detected at this time (Figs. 4A,D,G, 6A,B, and not shown). By E18, slit3 expression disappeared from the neocortex, whereas slit1 was still expressed in the cortical plate (Fig. 4B,E,H). This pattern was maintained until E20, when slit2 started to be detected at a low level in the cortical plate (not shown). From P5, all three *slits* were expressed, and their expression pattern was maintained to the adult. slit1 was confined to layers Va and VI (Fig. 4C), slit2 to layer V of the entire cortex and layers II and III of the cingular cortex (Fig. 4F), whereas slit3 was more broadly expressed in layers II-III, Va, and at a lower level in layer VI (Fig. 4I; Table 2),

Hippocampal formation

We previously described some aspects of the expression pattern of slit1, slit2, robo1, and robo2 in the developing hippocampus, until P5 (Nguyen-Ba-Charvet et al., 1999; see also Tables 1 and 2). We found that these four genes were still expressed in this structure later on. robo1 and robo2 expression was unchanged from P5 to the adult (Table 1). Both genes were highly expressed in pyramidal neurons of the CA1-CA3 subfields and in scattered neurons of the hilus (Fig. 5A,B). However, only robo2 was present in granule cells of the dentate gyrus (Fig. 5B) and in the subiculum (not shown). In contrast slit1 and slit2 expression pattern changed drastically between P10 and the adult. At P10, although slit1 was expressed at very high levels in the CA3 subfield (Fig. 5C) and weakly in other hippocampal regions, slit2 expression was strong in all hippocampal subfields (Fig. 5E). In the adult, slit1 expression was up-regulated throughout the hippocampus (Fig. 5D). In contrast, slit2 expression was down-regulated to very low levels except in the CA3 subfield (Fig. 5F). Therefore, slit1 and slit2 expression pattern switches between P10 and the adult. We also studied slit3 expression that had never been reported. Interestingly, from E13 to the adult, slit3 was highly expressed in the hippocampal formation (Fig. 6; Table 2). At E13, apart from the floor plate and the skin (Fig. 6A), slit3 expression in the forebrain was restricted to the primordium of the hippocampus (Fig. 6A). At E15, this expression has increased, but neurons were also labeled in the entorhinal cortex (Fig.

6B). At P1, it was clear that *slit3* was expressed at very high levels in all the hippocampal formation (Fig. 6C). This expression pattern was maintained in the adult (Fig. 6D), although by this stage, *slit3*-expressing neurons were found also outside the hippocampal formation.

Hypothalamus

Most cells in the hypothalamus become postmitotic between E13 to E18 (Altman and Bayer, 1978). During this period, robo and slit genes were not detected in ventricular (VZ) or subventricular (SVZ) zones. robo genes had a very restricted pattern of expression throughout the hypothalamus (Table 3): robo2 was only detected in the paraventricular hypothalamic nucleus (Pavh) from E15 (Fig. 7B), whereas robo1 was slightly expressed in Pavh from E20 and the ventromedial hypothalamic nucleus (VMH) from P10 (Fig. 7E). Slit genes have a more extended pattern of expression in the hypothalamus (Table 4) than robo genes. Particularly, slit1 was widely expressed in scattered cells of the preoptic, anterior, and lateral areas of the developing and adult hypothalamus (Fig. 7C,G). A high slit1 expression was also detected in the dorsomedial and dorsal part of VMH. In contrast, slit2 and slit3 were expressed in a restricted pattern. slit2 was detected in Pavh, VMH, and the ventricular lining where tanycytes are localized (Fig. 7D,H). Robust slit3 expression was detected at the level of the VMH, the arcuate nucleus, and tuberomamillary areas (Fig. 7I-K). In summary, robo and slit genes have distinct and overlapping patterns of expression in the hypothalamus.

Thalamus

Most cells in the dorsal thalamus (dTH) and ventral thalamus (vTH) become postmitotic between E13 and E17 (Altman and Bayer, 1988). E13 is the onset of neurogenesis for cells in the caudal dTH nuclei, whereas cells in rostral and medial dTH nuclei are generated 1-3 days later. Cells in the vTH are generated between E13 and E15 (Altman and Bayer, 1988). Although dTH has undergone some architectonic differentiation by E15, dTH nuclei cannot be easily distinguished. At this stage, most of the medial and anterior nuclei have not been generated. whereas posterior (median geniculate, MG), ventral (ventroposterior lateral and ventromedian nuclei, VPL, and VPM), and lateral (dorsal lateral geniculate, dLG) structures begins to parcellate. A strong robo2 expression was detected in the entire dTH, except in the VZ and SVZ (Fig. 7B), whereas robust robo1 expression was detected in VZ. SVZ, and the most medial domain of the dTH (Fig. 7A). As development proceeds, dTH nuclei can be distinguished. A high level of robo2 expression was maintained in most dTH nuclei until birth. Then, robo2 expression decreased sharply in sensory thalamic nuclei, while it is maintained in intralaminar and ventral nuclei (Fig. 7F). Whereas robo1 expression disappeared from VZ and SVZ, its expression was maintained in the intralaminar and paraventricular nuclei (Table 3). During the period of neurogenesis in vTH, robo genes were not detected in mitotic cells of the thalamic neuroepithelium. By E15, vTH has undergone considerable architectonic differentiation and it is possible to histologically distinguish vTH nuclei: the reticular nucleus (Rt), the zona incerta (Zi), the ventral lateral geniculate (vLG), and the subthalamic nucleus (Sth). Already at this stage, robo1 and robo2 were differentially expressed in patterns similar to those observed in

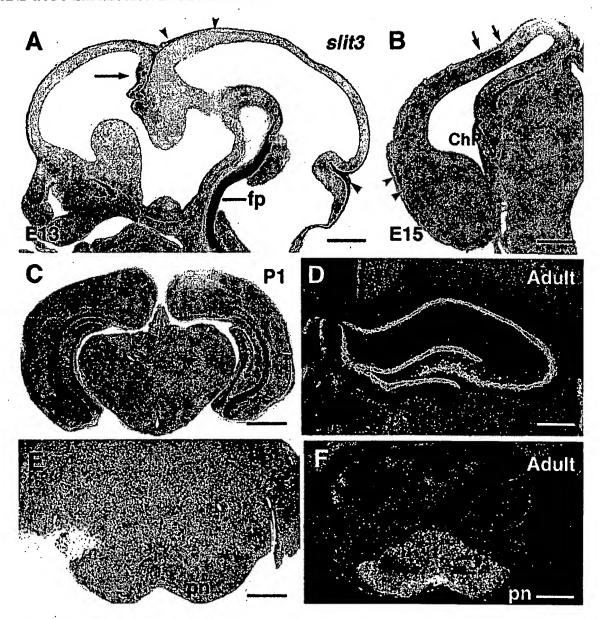


Fig. 6. slit3 expression in the developing hippocampal formation. Sagittal section (A) and coronal sections (B,C,E,F) were hybridized with digoxigenin-labeled riboprobes, whereas coronal sections (D,F) were hybridized with ³⁵S-labeled riboprobes. A: At embryonic day (E) 13, slit3 is expressed in the skin (arrowheads), the craniofacial mesenchyme (asterisk), the hippocampal primordium (arrow) and the floor plate (fp). B: At E15, slit3 is highly expressed in the developing hippocampus, the choroid plexus (ChP), the marginal zone of the

cortex (arrows) and the entorhinal cortex (arrowheads). C: At postnatal day (P) 1, a strong slit3 expression is detected in all the hippocampal system, including the entorhinal cortex. D: In the adult hippocampus, slit3 is strongly expressed in the pyramidal neurons of CA1 and CA3 subfields and in the granular cell layer of the dentate gyrus. E,F: Postnatally, slit3 is expressed in the pontine nuclei (pn) at P5 (E) and in the adult (F). Scale bars = 330 µm in A, 380 µm in B, 1,000 µm in C,F, 700 µm in D, 550 µm in E.

adults. robo2 was highly expressed in vLG, Rt, Sth nuclei, the rostral part of Zi, and most likely, at the level of A13 dopaminergic neurons (Fig. 7B,F; Table 3). robo1 expression pattern was far more discrete and was restricted to a subdomain of vLG and Sth (Fig. 7A,E; Table 3).

In summary, robo genes have distinct but overlapping expression patterns in subsets of dTH and vTH nuclei; the expression patterns often correlate with the histologically defined borders of nuclei. In addition, potential subdomains within the same nuclei (e.g., vLG) are suggested by some of the more discrete patterns.

Embryonically, *slit* genes had a very restricted pattern of expression in dTH. During the onset of dTH neurogenesis, from E13 to E18, robust *slit1* expression was only detected in the SVZ (Fig. 7C), whereas slight *slit2* expression was specifically detected in the VZ (Fig. 7D), possibly in radial glial cells. Postnatally, after major developmental events, *slit1* expression was detected in intralaminar, ventral, and lateral nuclei (Fig. 7G); *slit2* in anterior and posterior nuclei (Fig. 7H); and *slit3* in MG, dLG, laterodorsal (LD), lateroposterior (LP), and anterior nuclei (Fig. 7G,J,K; Table 4).

TABLE 3. Spatiotemporal Distribution of robo1 (1) and robo2 (2) mRNA in the Diencephalon1

Diencephalon	E15	E18	E20	P0	P5	P10	Adult
Hypothalamus	· · · · · · · · · · · · · · · · · · ·						
Ventromedial hypothalamic n.						1 –	1 -
Paraventricular n.	- 2	- 2	12	1 2	12	. 12	12
Eminencia thalamica	1 –						
Ventral thalamus				•			•
Ventral lateral geniculate n.	1 –	1 -	1 2	12	1 2	1 2	12
Reticular n.	12	12	12	1 2	12	1 2	12
Zona incerta	12	1 2	1 2				
Subthalamic n.	12	1 2	1 2	12	1 2	1 2	1 2
Dorsal thalamus				•			
Medial habenula	12	1 2	12	1 2	1 2	1 2	12
Intralaminar thalamic n.	1 –	1 2	12	12	1 2	1 2	12
Ventral medial n.		- 2	- 2	- 2	-2	1 2	12
Dorsal lateral geniculate n.	- 2	- 2				1-	1 –
Ventral basal n.	-2	- 2					
Lateral posterior and dorsal n.		- 2	- 2			1-	1 -
Median geniculate n.	-2	- 2	- 2	- 2		1 –	1 -
Median geniculate dorsal n.		- 2	- 2	-2		1 –	1 -
Paraventricular thalamic n.	1 -	1 -	1 2	1 2	1 2	1 2	. 12
Posterior n.		- 2	- 2	12	12	12	12
Pretectum							
Posterior commissure n.	1	1 2	1 -				

¹ E, embryonic day; P, postnatal day; n., nucleus; -, not detected.

In vTH, slit1 mRNA were detected from E15 at the level of A13 in Zi, from birth in Rt, and from P5 in Sth. Curiously, a sequential overlapping expression of slit genes was found in Rt (Table 4). Finally, slit3 was expressed in a subset of cells in vLG. In summary, slit genes have a distinct pattern of expression in the developing dTH, and they are most likely implicated in migratory events of newly dTH postmitotic neurons. robo1 and robo2 coexpression was also noted from E15 in the median habenula (mHb). From E15, whereas slit1 was expressed in the entire habenula, slit2 was only found in the mHb (Fig. 7C.D).

Mesencephalon

The neurons of the pars compacta and pars reticulata of the substantia nigra (SN) are generated between E13 and E15, whereas neurons of the ventral tegmental area (VTA) are produced between E14 and E16. From E15, robo1 was expressed in most of the postmitotic neurons of the SN-VTA complex, whereas robo2 was only found in SN neurons (Table 5). The levels of robo1 and robo2 expression

increased as development proceeds to reach a maximum by P10 (Fig. 8A,B). Interestingly, slit1 and slit2 coexpression began later in SN-VTA neurons (Fig. 8C,D; Table 6). Robo genes expression is maintained in adults with the concomitant expression of slit1 and slit2. The cytoarchitecture of the slits and robos coexpressing cells in the adult SN-VTA complex strongly indicates that theses ligands and receptors are coexpressed mainly in dopaminergic neurons: VTA and pars compacta (Fig. 8A-D), as well as in the caudal region of pars reticulata (not shown; Wassef et al., 1981).

Neurons were produced in the red nucleus between E13 and E14; in the periaqueductal gray (PAG) between E13 and E17; in the visual superior (SC) and auditory inferior (IC) colliculus between E14 and birth. We found that robo1 and robo2 were coexpressed in postmitotic neurons that form SC and IC. Whereas robo2 expression was maintained during postnatal life (Figs. 8B, 10B), robo1 expression stopped between birth and P5 (Figs. 8A, 10A; Table 5). Interestingly, in addition to IC, the other components of the auditory pathway, the cochlear nuclei, the lateral

pressed in the medial part of the habenula (mHb), and in the central lateral (CL), the central medial (CM) and the ventromedial (VM) thalamic nuclei. robo2 is also highly expressed in the lateroposterior nucleus (LP), the ventral lateral geniculate nucleus (vLG), and the reticular (Rt) and subthalamic (Sth) nuclei. G: At P10, slit1 is highly expressed in the medial part of the habenula (mHb) and much lower in the lateral part (lHb). slit1 is also strongly expressed in the laterodorsal nucleus (LD), in all intralaminar thalamic nuclei (PV, CL, VM, and CM), and the Rt. slit1 is also detected in the anterior (AH) and lateral (LH) area of the hypothalamus and in the lateral (LA) and medial (MA) nuclei of the amygdala. H: At P10, slit2 is highly expressed in the mHb, the choroid plexus (arrow), the ventromedial (VM) and Rt nuclei. In the hypothalamus, slit2 is only expressed in the ventromedial nuclei (VMH) and the ventricular zone (arrowhead). slit2 is also detected in the lateral (LA) and medial (MA) nuclei of the amygdala. I: At E18, slit3 is not detected in the thalamus and is only found in the VMH. J,K: In the adult, a high slit3 expression is maintained in the VMH, but slit3 is also weakly expressed in the arcuate nucleus (Ar). A weak expression of slit3 in the median geniculate nucleus (MG) is also observed. Scale bars = 400 µm in A-D, 1,100 µm in E-H,J,K, 500 µm in I.

Fig. 7. robos and slits expression in the developing diencephalon. Coronal sections were hybridized with digoxigenin-labeled riboprobes (A-D,I), or with ³⁵S-labeled riboprobes (E-H,J,K) for robo1 (A,E), robo2 (B,F), slit1 (C,G), slit2 (D,H), and slit3 (I-K). A: At embryonic day (E) 15, robo1 is detected in the epithalamus (Et), the medial part of the dorsal thalamus (dTH), and the ventral lateral geniculate nuclei (vLG). B: At E15, robo2 is strongly expressed in the dTH and the ventral thalamus (vTH). Note the lack of expression in the zona limitans (zli). robo2 is also observed in the paraventricular hypothalamic nuclei (Pavh) and in the dopaminergic cell group A13. C: At E15, slit1 is expressed in the medial habenula (mHb) and the subventricular zone of the dorsal thalamus (arrowhead). slit1 is also found in the dopaminergic cell group A13 and in the hypothalamus at the level of the dorsomedial nucleus (Dmh) and the periventricular hypothalamic area (Pe). D: At E15, slit2 was detected in the medial habenula (mHb) and the paraventricular hypothalamic nuclei (Pavh). E: At postnatal day (p) 10, robo1 is weakly expressed in the medial habenula (mHb), the central lateral nucleus (CL), the dorsolateral geniculate nuclei (dLG), the paraventricular nucleus of the thalamus (PV), and the subthalamic nucleus (Sth). robol is also detected in the basomedial nucleus of the amygdala (BM). F: At P10, robo2 is ex-

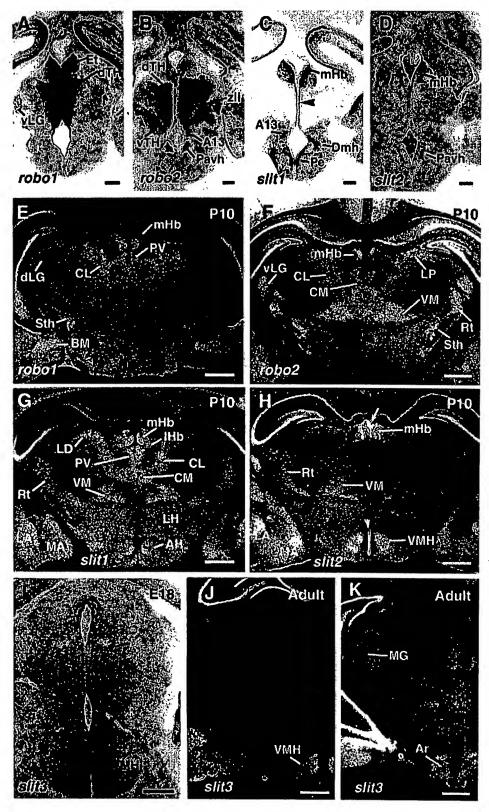


Figure 7

TABLE 4. Spatiotemporal Distribution of slit1 (1), slit2 (2), and slit3 (3) mRNA in the Diencephalon1

Diencephalon	E15	E18	E20	P0	P5	P10	Adult
Hypothalamus							
Ventromedial hypothalamic n.	- 2 -	-23	- 23	-23	-23	123	123
Paraventricular n.		-2 -	-2-	-2-	-2-	-2-	- 2 -
Anterior hypothalamic n.	1	1	1 '	. 1	1	1 – 3	1 – 3
Lateral hypothalamic n.	1	12	12	12	12	12-	12
Lateral preoptic area	1	1	1	1	1	1	1
Preoptic n.	-2-	-2-	-2-	-2-	-2-	-2-	- 2 -
Supraoptic n.	nd	nd	-2-	-2-	-2 -	-2 -	2-
Suprachiasmatic n.	nd	. nd	- 2 -	-2-	-2-	- 2 -	-2-
Ventral thalamus							
Ventral lateral geniculate n.						3	3
Reticular n.				12-	123	123	123
Zona incerta	1	1	1	1 – 3	1 – 3	1 – 3	1-3
Subthalamic n.				<u>-</u>	1	1	
Dorsal thalamus						1	
Medial habenula	12-	12-	12-	12-	12-	12-	12-
Lateral habenula	1	1	1	1	1	1	1
Anterior lateral and dorsal n.			-2-	-23	-23	-23	-2-
Intralaminar thalamic n.			. 			1	1
Ventral medial n.						123	1-3
Dorsal lateral geniculate n.						3	
Lateral posterior and dorsal n.						1-3	
Median geniculate n.							3
Median geniculate dorsal n.			·				3
Paraventricular thalamic n.							3
Posterior n.				-2-	-2-	-2-	
Pretectum		•					
Optic tract n.	nd	nd	nd	-2-	-2-	-2-	-2-

¹ E, embryonic day; P, postnatal day; n., nucleus; nd, not determined; -, not detected.

superior olive, the lemniscal nuclei, and the trapezoid nucleus displayed a robust *robo2* expression (Fig. 8E). We also found *robo2* gene expression in the red nucleus and in PAG (Table 5).

slit genes were expressed in a very limited pattern from E15. slit1 gene was detected in scattered cells of SC and IC (Fig. 10C), and slit2 was found in the red nucleus, PAG, and probably the serotonergic neurons of the raphe (Fig. 8F).

Other structures. We found that only slit2 was expressed in the pineal recess and the subcommissural organ (not shown), whereas both slit2 and slit3 were present in the choroid plexus (Figs. 4H, 6B, 10F).

Hindbrain

Cerebellar system. The expression patterns of slit and robo genes were particularly interesting in the cerebellum, where, to a large extent, they were expressed in different and often complementary structures. At E15, robo1 (Fig. 9A) and robo2 (Fig. 9D) expression was detected in zones corresponding, respectively, to masses of migrating deep nuclear neurons and Purkinje cells (Altman and Bayer, 1985; Feirabend, 1990). In contrast, a very low level of slit1 (Fig. 9G) and a high level of slit2 (Fig. 9J) mRNAs were expressed in the mantle layer, composed of migrating Purkinje cells (Altman and Bayer, 1985). Slit1 was also observed in a group of cells adjacent to the cerebellar plate (Fig. 9G) and possibly corresponding to the neurons of the parabrachial nucleus (Cholley et al., 1989). slit3 was not detectable in the embryonic cerebellum (Fig. 9M,N). At E18, the cerebellar cytoarchitecture was more mature and at that stage robo1 was still only expressed in deep nuclear neurons (Fig. 9B). In contrast, robo2 expression was confined to Purkinje cells (Fig. 9E) and, thus, complementary to robo1 expression. slit1 and slit3 were not detectable at E18 in the cerebellar plate (Fig. 9H,N; Table 6), whereas slit2 was found in subsets of deep nuclear neurons and Purkinje cells (Fig. 9K). This expression pattern was mostly unchanged until birth (Table 6). At P5, granule cells have started to migrate from the external granular layer (egl) and oligodendocytes have invaded the white matter. We found that robo1 was still expressed in the deep nuclei but that, in addition, it could be found in cells in the white matter, most likely glial cells (Fig. 9C; Table 5). robo1 expression in the white matter was transient and persisted only until P10 (not shown, Table 5). robo2 was also found from that stage in some deep nuclear neurons, but it was still highly expressed in all Purkinje cells, and at a low level in the granule cell layer (Fig. 9F). slit1 expression was now discernible but restricted to the deep nuclei (Fig. 9I). In contrast to a previous study (Liang et al., 1999), we could not detect any slit2 expression in the egl (Fig. 9L). slit2 mRNA was found in small subsets of deep nuclear neurons and in subsets of Purkinje cells (Fig. 9L) in the vestibulocerebellum (uvula, nodulus, flocculus, and paraflocculus). At this stage, a low level of slit3 expression started to be detectable in the granule cell layer (Fig. 90). To a few noticeable exceptions, this expression pattern was maintained in the adult cerebellum. robo1 and robo2 were expressed in all subdivisions of the deep nuclei (Fig. 10A,B and not shown). Robo2 was also expressed in all Purkinje cells but also in Golgi cells in the granule cell layer (Fig. 10B,G). slit1 expression was very low and restricted to the lateral and interpositus deep nuclei (Fig. 10C, not shown; Table 6). slit2 was also expressed in the lateral and interpositus nuclei and also in Purkinje cells in the vestibulocerebellum (Fig. 10D,F). In the adult cerebellum, slit3 was very highly expressed in granule cells (Fig. 10E,H) and in the lateral cerebellar nuclei (not shown, Table 6).

Inferior olive. We studied in detail slits and robos expression in inferior olivary (IO) neurons, which project as climbing fibers to Purkinje cells and deep nuclear neurons in the cerebellum. At E15, when IO neurons have just finished their tangential migration from the rhombic lip. robo1 and robo2 expressions were diffuse in the brainstem. Nevertheless, most IO neurons expressed high level

TABLE 5. Spatiotemporal Distribution of robo1 (1) and robo2 (2) mRNA in the Mesencephalon and Rhombencephalon1

Mesencephalon and							
rhombencephalon	E15	E18	E20	P0	P5	P10	Adult
Substantia nigra	1 2	12 .	1 2	1 2	12	12	1 2
Ventral tegmental area	1 -	1-	1 –	1 –	1 -	1 -	1 -
Superior colliculus	1 2	12	1 2	- 2	2	- 2	- 2
Deep n.	– nd	- 2	- 2	- 2	- 2	- 2	-2
Red n.	- nd	- 2	- 2	- 2	- 2	- 2	- 2
Cuneate n.	. nd	12	1 2	1 2	12	1 2	1 2
Gracile n.	nd	12	1 2	1 2	12	1 2	12
Pontine n.				- 2	- 2	- 2	- 2
Motor nuclei	•					= ,	-
Oculomotor n. (III)							
Trochlear n. (IV)							
Trigeminal n. (Vm)		1-	1 -	1 -	1 -	1 –	1 -
Abducens n. (VI)	nd	nd	nd	nd	nd	ī -	i-
Facial n. (VII)	1 -	1-	1 -	1 -	i –	i -	i -
Vagus n. (X)	1	1-	1 -	<u>-</u> -			
Hypoglossal n(XII)	12	12	1 2	1 2	12	12	12
Sensory nuclei				,		• •	1 2
Spinal trigeminal n. (Vs)	nd	- 2	- 2	·-2	 2	- 2	- 2
Cochlear n. (VIII)	nd	1 2	1 2	1 2	12	12	12
Vestibular n. (VIII)	nd	12	1 2	12	12	12.	12
Auditory pathway					,		12
Inferior colliculus	12	12	12	-2	- 2	-2	- 2
Lateral superior olive				- 2	- 2	-2	-2
Lemniscal n.	nd	-2	- 2	-2	- 2	-2	2
Trapezoid n.	nd	- 2	- ž	-2	-2	- 2 - 2	-2
Cerebellum		_	-	-		7.2	- 2
Purkinje cells	- 2	- 2	- 2	-2	- 2	- 2	- 2
Deep nuclei	1-	1-	1 2	1 2	12	12	12
Granule cells	-	-	- 		2	-2	-2
White matter					1-	1-	2
Inferior clivary complex					• =	1-	
Medial accessory olivary n.	- 2	- 2	- 2	- 2	- 2	- 2	- 2
Dorsal accessory olivary n.	- 2	- 2	- Ž	- 2	1 2	12	12
Principal olivary n.						-2	-2

¹ E, embryonic day; P, postnatal day; n., nucleus; nd, not determined; -, not detected.

of robo2 mRNA whereas robo1 labeling was hardly above background (Fig. 11A,D). Similarly, at this stage, slit1 and slit3 were weakly expressed in the IO, whereas slit2 was not detectable (Fig. 11G,J,M). This expression pattern was unchanged until birth, when the olivary cytoarchitecture has already reached a mature appearance, thus, making it possible to determine which IO subnuclei express the different genes. At P1, robo1 expression was still undetectable (Fig. 11B; Table 5), whereas robo2 was highly expressed in the medial and dorsal accessory olive (MAO and DAO) and a large portion of the principal olive (PO; see Fig. 11E; Table 6). slit1 transcripts were found in the PO and rostral MAO (Fig. 11H), slit2 was not expressed, and slit3 was detected at a low level throughout the IO (Fig. 11K,N; Table 6). From P10, the expression pattern was unchanged: there was a weak robo1 expression in the DAO (Fig. 11C), whereas robo2 was expressed in all IO neurons (Fig. 11F). slit2 was not expressed in the IO, slit1 was confined to the DAO and PO, but slit3 was expressed in all IO subdivisions (Fig. 11I,L,O). In addition, at this stage, other precerebellar nuclei, which send mossy fibers to the cerebellar cortex, also clearly expressed some slit and robo genes. For instance, the lateral reticular nucleus expressed high levels of slit2 and slit3 (Fig. 11L,O), and pontine neurons expressed slit3 and robo2 mRNAs from the birth (not shown, and Fig. 6E,F).

Sensory and motor nuclei. In the medulla, cranial motor neurons are generated between E12 and E13 and neurons in brainstem sensory nuclei are generated slightly later between E13 and E15. Cranial motor neuron nuclei project to peripheral targets, whereas sensory nuclei project in a very precise topographic manner to the somatosensory thalamus (VPM and VPL). We also found

that robo genes were expressed in a distinct and almost complementary pattern; robo1 was only expressed in cranial motor nuclei from E13, whereas from E15–E18, robo2 was expressed by sensory nuclei (Fig. 11B–F; Table 5). However, robo2 was also expressed by hypoglossal motor neurons (Fig. 11D,E). We found that slit1, slit2, and slit3 were expressed in some cranial motor neurons (Fig. 11J–L; Table 6).

DISCUSSION

In this study, we provide the first comprehensive study of *slit* and *robo* gene expression in the developing and adult rat brain. We found that each of these genes is expressed in a unique spatiotemporal pattern. This analysis suggests that Slits and Robos are involved in multiple aspects of the development of many classes of neurons. It also underlines that our understanding of Slit and Robo functions is still incomplete.

To date, Slit and Robo function has been mostly studied in *Drosophila* embryos. In *Drosophila*, Slit is expressed by non-neuronal cells such as midline glia or muscle attachment sites, and regulates midline crossing by developing axons and the migration of muscle precursors (Rothberg et al., 1990; Kramer et al., 2001). For the latest, Slit is bifunctional, i.e., repulsive or attractive (Kramer et al., 2001). We found that in the rat CNS, like in *Drosophila*, slit genes are all expressed at the ventral midline in floor plate cells, but unlike *Drosophila*, they do not appear to be in glial cells. (This observation requires further confirmation by double staining with glial cell markers.) Likewise, robos are only found in neurons, with no apparent correlation between their temporal expression pattern and the

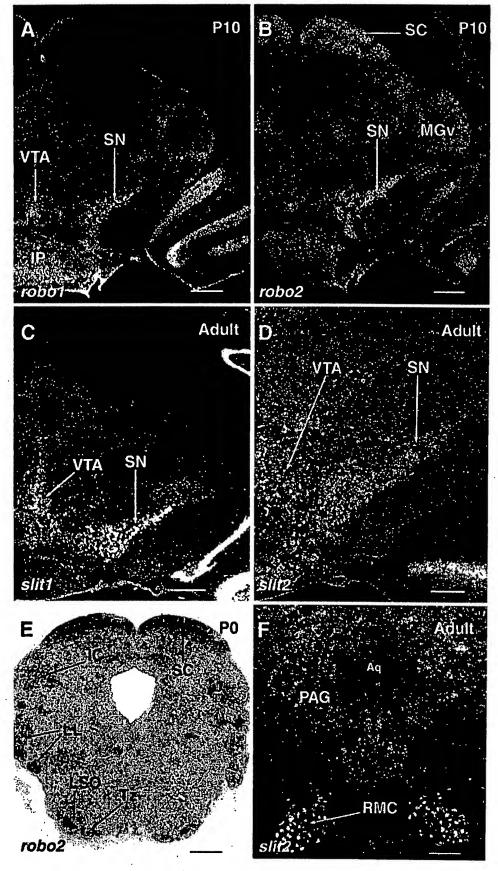


Fig. 8. robos and slits expression in the developing mesencephalon. Coronal sections were hybridized with digoxigenin-labeled riboprobe (E), or with ⁸⁶S-labeled riboprobes (A-D,F) for robo1 (A), robo2 (B,E), slit1 (C), and slit2 (D,F). A: At postnatal day (P) 10, robo1 is strongly expressed in the substantia nigra pars compacta (SN), the ventral tegmental area (VTA), and in the interpeduncular nucleus (IP). B: At P10, robo2 is highly detected in the superior colliculus (SC), the substantia nigra pars compacta (SN), and weakly in the ventral median geniculate nucleus (MGv). C,D: In the adult, slit1 and slit2

are strongly expressed in the SN pars compacta and the ventral tegmental area (VTA). E: At P0, robo2 is found in all the auditory relays: the inferior colliculus (IC), the lateral lemniscal nucleus (LL), the lateral superior olive (LSO), and the trapezoid body nucleus (Tz). robo2 is also highly expressed in the superficial layer of the superior colliculus (SC). F: In the adult, slit2 is detected in the periaqueductal gray (PAG) and the red magnocellularis nucleus (RMC). Aq, aqueduct. Scale bars = 660 μm in A,B, 320 μm in C,D,F, 550 μm in E.

TABLE 6. Regional Distribution of slit1 (1), slit2 (2), and slit3 (3) mRNA in the Mesencephalon and Rhombencephalon 1

Mesencephalon and rhombencephalon	E15	. E18	E20	P0	P5	P10	Adult
Substantia nigra						1	12-
Ventral tegmental area						1	1
Superior colliculus	1	1	1	1	1	1	1
Red n.	-2-	-2-	2-	- 2 -	- 2 -	-2-	-2-
Inferior colliculus	1	1 –	1	1	1	1	1
Raphe n.	-2-	- 2 -	- 2 -	- 2 -	-2-	12-	12-
Pontine n.				3	3	3	3
Motor nuclei							
Oculomotor n. (III)	-23	-23	-23	- 3	-3	- 3	- 3
Trochlear n. (IV)	3	- 2 3	- 3	- 3	- 3	- 3	- 3
Trigeminal n. (Vm)	123	23	23	2 3	2 3	23	23
Abducens n. (VI)	nd	nd	nd	nd	nd	-23	-23
Facial n. (VII)	-23	- 2 3	- 2 3	-23	-23	-23	-23
Vagus n. (X)	3 '	3	3	3	3	3	3
Hypoglossal n. (XII)	123	123	123	. 123	123	123	123
Sensory nuclei							
Spinal trigeminal n. (Vs)	nd						
Cochlear n. (VIII)	nd	1	1	1	1	1	1-3
Vestibular n. (VIII)	nd	12-	· 1 2 -	12-	12-	123	123
Cerebellum				•			
Purkinje cells	-2-	- 2 -	- 2 -	- 2 -	2-	-2-	-2-
Deep nuclei	1	1	1	12-	123	123	123
Granule cells					3	8	3
Inferior clivary complex						·	_
Medial accessory olivary n.	1	1	1	1 - 3	1 – 3	1-3	1 - 3
Dorsal accessory olivary n.	. 1	1	1	1 – 3	1-3	1-3	1-3
Principal olivary n.	Ī	1	1	1 – 3	1-3	1-3	1-3

¹ E, embryonic day; P, postnatal day; n., nucleus; nd, not determined; -, not detected.

crossing or noncrossing of the CNS midline by their axons. This finding suggests that these molecules play multiple roles in the control of CNS development.

Our study revealed that most CNS neurons express at least one robo and one slit gene during their development. The only noticeable exceptions to this rule being the septum (where no robos were detected), layer IV neurons in the neocortex, and dispersed reticular neurons in the brainstem. Some neurons express only one slit gene. This is the case for neurons in the olfactory epithelium, the lateral habenula, the hypothalamus, or the superior and inferior colliculi, which express only slit1. Similarly, cerebellar Purkinje cells and supraotic and suprachiasmatic neurons in the hypothalamus express only slit2, whereas cerebellar granule cells and motor neurons of the vagus nerve express only slit3. Nonetheless, in most systems, neurons express multiple slit genes simultaneously, sometimes (e.g., in the hippocampus) at different periods of their development. At the extreme, CA3, entorhinal cortex, hypoglossus, and layer V neurons among others, coexpress the three slit genes from E15 to the adult. In most cases, slit expression is up-regulated after P10 such as the three slit genes are simultaneously express only when neurons have reached the adult stage.

Likewise, most neurons express a single robo gene, either robo1 (olfactory tubercle, indusium griseum, ventral tegmental area, and so on) or more often robo2 (most sensory related neurons, Purkinje cells, pons, subiculum, and so on). However, some coexpress, robo1 and robo2, such as in the substantia nigra, hypoglossus, or striatum. Interestingly, robo's expression pattern is less dynamic than slits, and with a few exceptions (olfactory tubercle and accessory olfactory bulb), it does not evolve much between E15 and the adult. Another interesting aspect of slit and robo expression patterns is that in several systems, and particularly at embryonic stages, these genes are expressed in a complementary manner. For instance, in the embryonic cerebellum, Purkinje cells express robo2

and slit2, whereas their target cells in the cerebellum, the deep nuclear neurons, express robo1 and slit1. Similarly, in the E15 cerebral cortex, robo1 is in the cortical plate and robo2 in the intermediate and subventricular zones.

slit3 expression pattern is rather unique. From E13 to birth it is found almost exclusively in the hippocampal formation, whereas other slits are more widely expressed. The onset of slit3 expression coincides with the first delineation of the hippocampal primordium and is maintained in the hippocampal formation until the adult stage. slit3 is one of the first genes selectively expressed in the embryonic hippocampal formation, suggesting that Slit3 has an important function in the development of this system. For instance, it might regulate the formation of neuronal connections and/or the specification of the hippocampal region. Several genes also expressed in the embryonic hippocampal primordium have been identified, some of which code for transcription factors (Tole et al., 1997; Grove and Tole, 1999; Tole and Grove, 2001). This finding led to the hypothesis that the pole of the hippocampal primordium close to the midline, the so-called cortical hem, is an organizer of the hippocampal field, producing diffusible inductive factors, and Slit3 could participate to this process.

Role for Slits and Robos in projection map formation

In the CNS, most axons do not terminate randomly in their target territory but are precisely organized, with a specific topography, and form the so-called projection maps. One of the major conclusions of our study is the spatiotemporal coincidence of *robo* expression in developing structures that project abroad long distances and in a highly ordered pattern. In particular, *robo2* expression is tightly associated to developing sensory systems (olfactory, visual, auditory, and somatosensory) during the critical period of sensory axons outgrowth and pathfinding to the CNS *robo2* is expressed in all sensory-related stations of

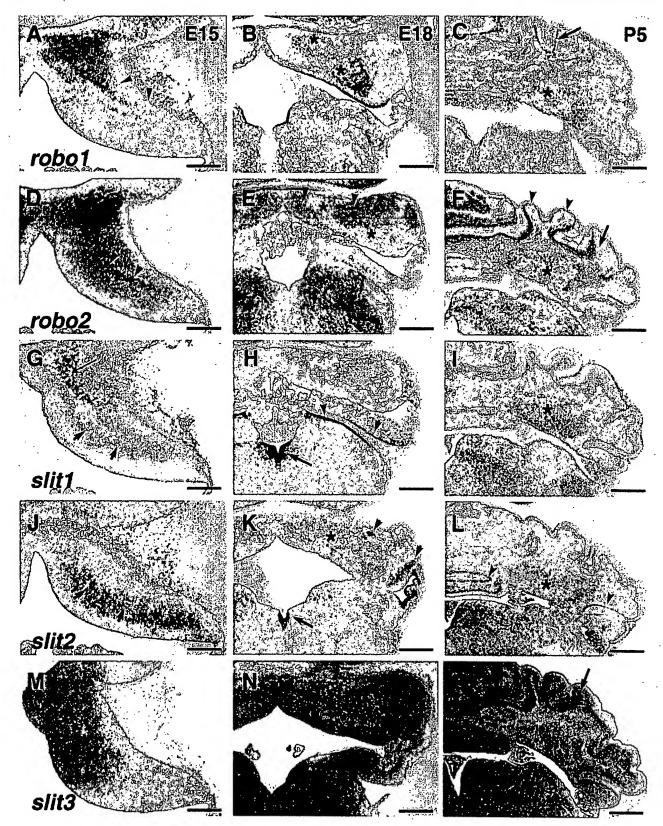


Figure 9

the CNS during their period of axonal pathfinding. For instance, in the visual system, robo2 is expressed from E15 in retinal ganglion cells, in the primary visual thalamic relay, the dorsal lateral geniculate nucleus and in the superior colliculus. Moreover, in vitro studies have shown that Slit2 repels developing retinal and thalamic axons (Erskine et al., 2000; Niclou et al., 2000; Ringstedt et al., 2000). In the auditory system, we find that robo2 is expressed during the period of axonal pathfinding of auditory related peripheral and central structures, the cochlea, the cochlear nuclei, the inferior colliculus, the lateral superior olive, the trapezoid body nucleus, and the thalamic median geniculate nucleus. Similarly, in the somatosensory system, robo2 is expressed during the period of axonal pathfinding of somatosensory-related structures, the trigeminal ganglion, the dorsal root ganglia, the cuneate and gracile nuclei, the three spinal trigeminal nuclei (principalis, oralis, and interpolaris), and the thalamic ventroposterior medial and lateral nuclei. Taken together, we can propose that Robo2 participates to the guidance of all primary sensory and central sensoryrelated axons. robo2, which is also expressed in most components of the motor system (layer V of the motor cortex, basal ganglia, ventromedial nucleus of the thalamus, red nucleus, basilar pons, cerebellum, inferior olive, motor nuclei) could also control the guidance of motor-related axons in the CNS.

In some systems, there is a good correlation between slits and robos expression. In the accessory olfactory system, where the apical and basal zones of the vomeronasal organ are mapped, respectively, to rostral and caudal domains of the accessory olfactory bulb (Mori et al., 2000), slit1 and robo2 are expressed topographically. robo2 is expressed in the basal zone of the VNO, whereas slit1 is restricted to the apical part of the VNO, which suggests that these two molecules might participate to the organization of this projection possibly by restricting the mixing

Fig. 9. robos and slits expression in the developing cerebellum. Coronal sections were hybridized with digoxigenin-labeled riboprobes for robo1 (A-C), robo2 (D-F), slit1 (G-I), slit2 (J-L), and slit3 (M,N). A: At embryonic day (E) 15, robol is detected in migrating deep nuclear neurons (arrowheads). B: At E15, robo1 is only expressed in neurons of the deep nuclei (asterisks). C: At postnatal day (P) 5, robo1 is still found in the deep nuclei (asterisk), and in glial cells of the cerebellar white matter (arrow). D: At E15, robo2 is also expressed in migrating Purkinje cells (arrowheads). E: At E18, robo2 is specifically found in Purkinje cells (arrowheads) and is not detected in the deep nuclei (asterisks). F: At P5, robo2 expression is maintained in Purkinje cells (arrowheads). However, robo2 is also present in some cells of the deep nuclei (asterisk) and at a low level in the granular cell layer (arrow). G: At E15, a very low level of slit1 is found in the migrating Purkinje cells of the mantle layer (short arrows) and in migrating cells (long arrow) probably cells of the parabrachial nucleus. H: At E18, slit 1 is not detectable in the cerebellum, but it can be observed in the rhombic lip (arrowheads) and in the floor plate (arrow). I: At P5, slit1 is expressed in the deep nuclei (asterisk). J: At E15, at a high level of slit2 mRNAs is expressed in migrating Purkinje cells of the mantle layer (short arrows). K: At E18, slit2 is expressed in subsets of deep nuclear neurons (asterisk) and subsets of Purkinje cells (arrowheads). slit2 is also present in the floor plate (arrow). L: At P5, slit2 is expressed in small subsets of deep nuclei (asterisk) and Purkinje cells in the vestibulo-cerebellum (arrowheads). M,N: slit3 is not detected from E15 (M) to E18 (N) in the cerebellum. O: At P5, a low level of slit3 was detectable in the granule cell layer (arrow). Scale bars = 230 μ m in A,D,G,J,M, 420 μ m in B,E,H,K,N, 600 μ m in C,F,I,L,O.

between the two populations of axons. robo1 and robo2 are also expressed in the AOB, but it is still unclear whether their expression is restricted to some domains.

Another example is the olivocerebellar system where inferior olivary neurons, in the medulla oblongata, send axons to Purkinje cells in the cerebellar cortex. This projection is arranged according to a precise spatial order resulting from the segregation of olivary axons (the climbing fibers) into distinct compartments of Purkinje cells forming adjacent parasagittal bands. Studies on the development of the olivocerebellar system in vertebrates have revealed that, before the entry of olivary fibers into the cerebellum, there is a simultaneous, independent, and transient biochemical parcellation of the cerebellar cortex and the inferior olive (Sotelo and Chédotal, 1997). Therefore, we have suggested that the major mechanism involved in the formation of the olivocerebellar topography is the existence of matched positional or guidance cues between clusters of PCs and corresponding clusters of IO neurons (Sotelo and Chédotal, 1997). Our results suggest that Slits and Robos could be involved in the targeting of inferior olivary axons. From E15, when inferior olivary axons enter the cerebellar primordium (Wassef et al., 1992), robo2 is expressed by subsets of inferior olivary neurons, and slit2 by subsets of Purkinje cells in the vestibulocerebellum. Moreover, deep nuclear neurons, which are the targets of PCs axons and also of inferior olivary axon collaterals, also expressed combination of slits and robos.

Are Slits and Robos involved in neuronal migration?

In rodents, Slit1 and Slit2 are thought to play a role in the tangential migration of telencephalic interneurons. For instance, in diffusion assays, Slit1 and Slit2 are very potent repellents for neuroblasts produced in the subventricular zone and migrating along the rostral migratory stream (RMS) to the olfactory bulb (Hu, 1999; Wu et al., 1999). Similar studies have shown that GABAergic interneurons, migrating from the medial ganglionic eminence to the neocortex are also repelled by Slit1 and Slit2 (Zhu et al., 1999). In those two cases, if the involvement of Slit proteins seems convincing, the expression of robo receptors by the migrating neurons had not been demonstrated. We found that neuronal cells born in the postnatal telencephalic subventricular zone display a strong robo2 expression and a weak robo1 expression from their entrance in RMS to their arrival in the olfactory bulb, which suggests a role of the couple slits/robos in the control of this migration. In the meantime, we found that these migrating cells, specially in the adult brain, also express high levels of slit1 mRNA, suggesting that Slit1 exerts additional functions in this system, and may act in an autocrine manner (see below), possibly by influencing the proliferation or the differentiation of these cells. Moreover, we could not detect any robo expression in cells migrating through the ganglionic eminences to the neocortex, which does not support a role for Robo1 or Robo2 in the control of the migration of these neurons in vivo. A possibility could be that, in this system, slit function is mediated by another receptor (see below).

Other expression data support a role for Slit and Robo, and more precisely Robo2, in the control of tangential migration. In the hindbrain, precerebellar neurons, of the inferior olive and pontine nuclei, migrate tangentially to-

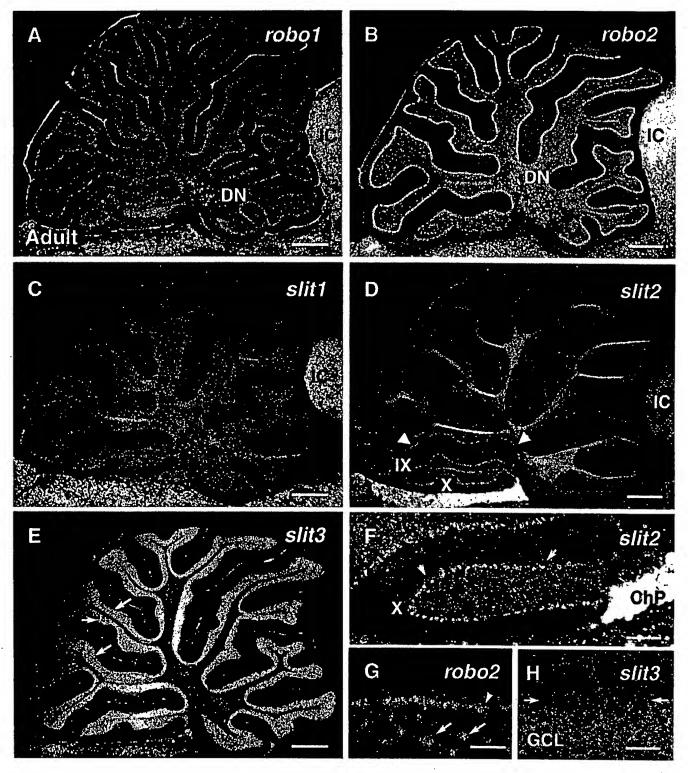


Fig. 10. robos and slits expression in the adult cerebellum. Sagittal sections (A-H) were hybridized with ³⁵S-labeled riboprobes for robo1 (A), robo2 (B,G), slit1 (C), slit2 (D,F), and slit3 (E,H). A: robo1 is expressed in all the deep nuclear neurons (DN). B: robo2 is highly expressed in all Purkinje cells, deep nuclear neurons (DN), and Golgi cells. C: slit1 is absent of the adult cerebellum. D: slit2 is specifically detected in Purkinje cells of the lobules IX and X (arrowheads). E: slit3 is highly expressed in the granular cell layer (arrows).

F: Higher magnification of slit2 expression in Purkinje cells of the lobule X (short arrows). G: Higher magnification of robo2 expression in Purkinje cells (arrowhead) and Golgi cells (short arrows). H: Higher magnification of slit3 expression in granular cell layer (GCL) of the cerebellum. The short arrows indicate the Purkinje cell layer. IC, inferior colliculus; ChP, choroid plexus. Scale bars = 890 µm in A-E, 240 µm in F, 180 µm in G, 60 µm in H.

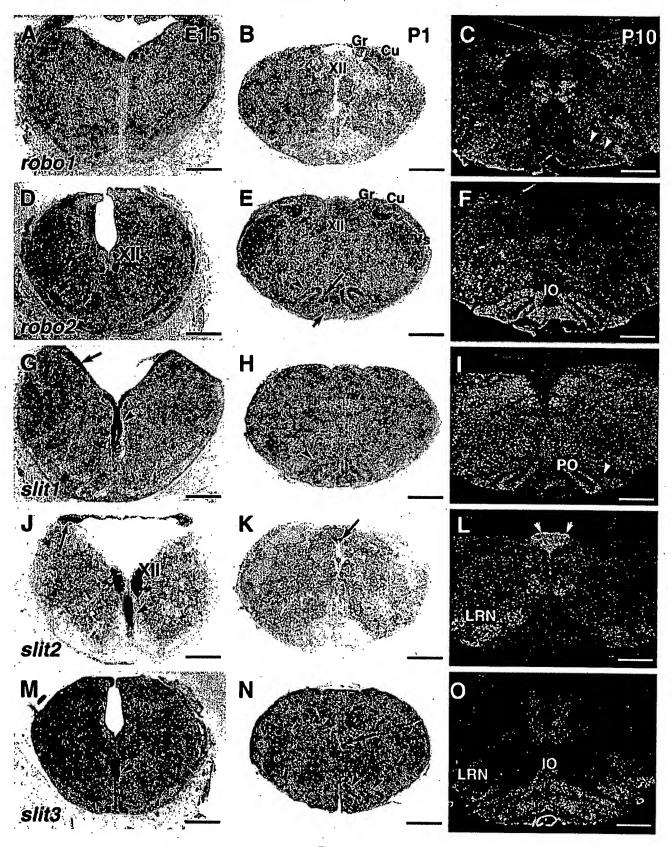


Figure 11

ward the floor plate. During their migration, these neurons express robo2, whereas slit1, slit2, and slit3 are found in the floor plate. Interestingly, their migration is known to be under the control of netrin-1 (Bloch-Gallego et al., 1999; Yee et al., 1999; Alcantara et al., 2000), another diffusible factor, which can bind to Slit and whose receptor DCC has just been shown to interact with Robo (Stein and Tessier-Lavigne, 2001). It is therefore likely that slits and netrin-1, which are essential for the control of midline crossing by developing axons, cooperate to control the tangential migration of precerebellar neurons.

Our study reveals that robo2 is expressed in the embryonic olfactory epithelium but also in cells migrating away from this epithelium (De Carlos et al., 1995). During development, three distinct cell types migrate from the olfactory epithelium and, thus, might express robo2: the glial ensheathing cells, the LHRH-producing cells, and some olfactory marker protein (OMP)-immunoreactive cells (De Carlos et al., 1995). Glial ensheathing cells contribute to the development of olfactory glomeruli (De Carlos et al., 1995). LHRH neurons migrate through the forebrain to their final destination in the septal preoptic nuclei and hypothalamus (Schwanzel-Fukuda and Pfaff, 1989). OMP-immunoreactive cells migrate to the ventrolateral part of the olfactory bulb (De Carlos et al., 1995). Because slit1 and slit2 are expressed in cells lining the pathway followed by the migrating cells (the midline mesenchymal cells, the olfactory epithelium, the olfactory bulb, the basal forebrain, and so on), Slit/Robo could be involved in the control of the migration of these cells.

Role of Slits and Robos in axonal branching

Several axon guidance molecules are also branching factors (see for a review Kalil et al., 2000). Slit2 was originally isolated in vertebrate as a branching factor for NGF-responsive sensory axons of the dorsal root ganglia (Wang et al., 1999). It is not known yet whether Slit2 has

Fig. 11 (Overleaf). robos and slits expression in the developing olivary system. Coronal sections were hybridized with digoxigeninlabeled riboprobes (A,B,D,E,G,H,J,K,M,N) or with 35S-labeled riboprobes (C,F,I,L,O) for robo1 (A-C), robo2 (D-F), slit1 (G-I), slit2 (J-L), and slit3 (M-O). A-C: At embryonic day (E) 15 (A), robo1 is not detected in inferior olivary neurons, and at postnatal day (P) 1 (B) robol expression is still undetectable in this structure. From postnatal day (P) 10 (C), a low level of robo1 is found in the dorsal accessory olive (arrowheads). A weak robo1 expression is observed in the hypoglossal (XII), the cuneate (Cu), and gracile (Gr) nuclei from P1. D-F: At E15 (D), robo2 is strongly expressed in migrating olivary neurons in the tangential migratory stream (short arrows). From P1 (E) to P10 (F), robo2 is highly detected in the medial and dorsal accessory olive (arrowhead) a large portion of the principal olive (long arrow) and in the medial accessory olive (short arrow). robo2 is also observed in the hypoglossal nucleus (XII), the spinal trigeminal nuclei (Vs), and the cuneate (Cu) and the gracile (Gr) nuclei. G-I: At E15 (G), slit1 is detected in the rhombic lip (arrow) and in the floor plate (arrowhead). From P1 (H), slit1 starts to be detected in the principal olive (PO) and the dorsal accessory olive (arrowhead in H and I). J-L: From E15 (J) to P10 (L), slit2 is highly expressed in the hypoglossal nucleus (XII), the lateral reticular nucleus (LRN), the area postrema (arrowheads in L), the rhombic lip (arrow in J), in the floor plate at E15 (arrowhead in J), and in the roof plate (arrow in K). M-O: At E15 (M), slit3 is only detected in the floor plate (short arrow). From P1 (N) to P10 (O), slit3 is also expressed in the inferior olive (IO) (arrowheads in N), the hypoglossal (arrow in N) and the lateral reticular (LRN) nuclei. Scale bars = 300 μ m in A,D,G,J,M, 670 μ m in B,C,E,F,H,I,K,L,N,O.

as a similar branching activity on other classes of axons, neither is it known whether other slits have branching activities. In the CNS, axonal branching has been mostly studied in the corticopontine projection. In this system, layer V neurons of the motor cortex initially project into the spinal cord and later send axon collaterals to their final target, the basilar pons, by a process of interstitial branching (O'Leary et al., 1990, 1991). Coculture experiments in collagen gels have shown that these axonal branches are attracted toward the pons by a diffusible factor that has not been identified yet (Heffner et al., 1990). We found that during this branching period (occurring between birth and P2 in vivo) layer V neurons express robo1 and robo2 mRNAs and that the basilar pons expresses high levels of slit3. Therefore, it will be interesting to test directly whether Slit3 can stimulate branch formation in this system.

Slits and Robos function in the adult brain

A surprising result of our study is the clear demonstration that the expression of *slits* and their receptors is up-regulated during postnatal development and maintained at high levels in adult neurons. This up-regulation suggests that the function of these proteins is not restricted to the control of axonal pathfinding and neuronal migration but that they could also be involved in synaptic plasticity. The hippocampus is such a structure where persistent changes in connectivity have been observed and are correlated with modifications of neural activity (Toni et al., 1999). Interestingly, *slit1* and *robo2* expression patterns in the hippocampus change abruptly from P10, when synaptogenesis increases in this system (Steward and Falk, 1991).

In the adult CNS, injured neurons are not able to regenerate their axons. Myelin and proteoglycans are the best identified inhibitory molecules preventing axon regeneration, but chemorepulsive factors have also been proposed to play a role in this process (Pasterkamp et al., 2000). We could not obtained any evidence for *slits* expression in oligodendrocytes or astrocytes, which would argue against a role for these molecules in the inhibition of regeneration, although it could be possible that glial cells express them after a lesion.

CONCLUDING REMARKS

Most neurons simultaneously express slit and robo genes. It has been shown that there is a promiscuous binding of Slits to the different Robos (Brose et al., 1999; Li et al., 1999; A.C., K.T.N.-B.-C. and M.T.L. unpublished observation). For instance, in Drosophila, Slit is able to activate all Robos (Rajagopalan et al., 2000a,b; Simpson et al., 2000a,b). Therefore, our observations suggest that, in many systems, Slits could act in an autocrine manner, but this possibility requires direct testing. Such a coexpression of a diffusible factor and its receptors and a possible autocrine action has been proposed before for Slit2 in the developing spinal cord (Brose et al., 1999; Wang et al., 1999), and for members of the Semaphorin family (Shepherd et al., 1997; William-Hogargth et al., 2000). However, it was shown that, although all secreted semaphorins can bind with similar affinity to the neuropilin-1 (Chen et al., 1997), only a few of them are active on neuropilin-1 expressing axons and that coreceptors (the plexins) are required to specify the response (Takahashi et al., 1999; Tamagnone et al., 1999). In mammals, no direct proof has been obtained yet demonstrating the involvement of Robos in mediating all Slit actions. Moreover, Slits are also ligands of the heparan sulfate proteoglycan glypican-1 (Liang et al., 1999; Ronca et al., 2001), which is also expressed in developing neurons (Karthikeyan et al., 1994). It is likely that the slit receptor is a multimeric complex, and that understanding slit/robo function will require identifying and studying the expression pattern of these coreceptors that could modulate slit function. Several recent studies support this idea, as Robos have been shown to interact with the netrin receptor DCC (Stein and Tessier-Lavigne, 2001) and with the chemokine receptor CXCR4 (Wu et al., 2001). We have also shown that the response of sensory axons to Slit2 is modulated by extracellular matrix proteins such as laminin (Nguyen-Ba-Charvet et al., 2001b).

An important limitation to the analysis of slit/robo function in the vertebrate brain is the absence of antibodies allowing to visualize the subcellular location of slit and robo proteins. This is crucial, as in Drosophila, a key element in Robo function is the regulation of its expression on the growth cone by transmembrane proteins of the Commissureless family (Comm; Tear et al., 1996; Kidd et al., 1998b; Rajagopalan et al., 2000a; Simpson et al., 2000b). Comm acts posttranscriptionally to maintain Robo expression at a low level on the cell membrane of commissural axons until they have crossed the CNS midline. The exact mechanism of action of Comm is still unknown, and to date no Comm homologues have been identified in vertebrates. If such homologues exist, neurons expressing robo mRNAs could still be unresponsive to Slit. Recently, the phenotype of a Zebrafish mutant of the robo2 homologue, astray, has been reported and confirmed that this receptor is crucial for axonal pathfinding at the CNS midline. It is clear that an important step toward the understanding of slit/robo function in mammals will come from the analysis of robo and slit mutants.

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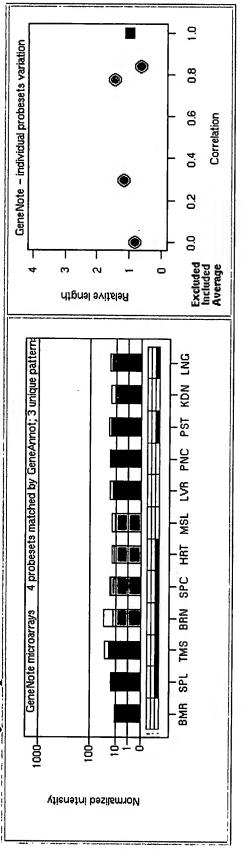
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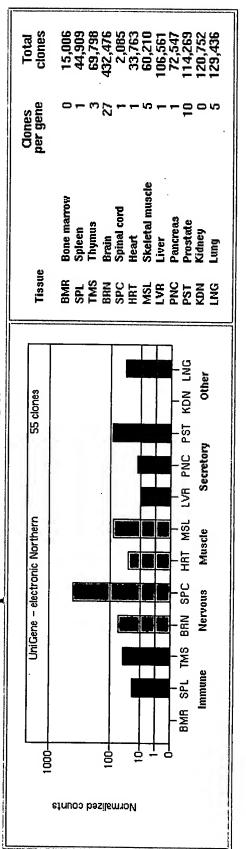
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Appendix B

Microarray Expression for ROBO1



Electronic Northern Expression for ROBO1



Microarrays

RNA source

PolyA+ RNA samples from twelve normal human tissues were purchased from Clontech (Palo Alto, CA). This collection of major human tissues includes:

pancreas (6539-1), prostate (6546-1), skeletal muscle (6541-1), spinal cord (6593-1), spleen (6542-1) and thymus (6536-1). Bone marrow (catalog number: 6573-1), brain (6516-1), heart (6533-1), kidney (6538-1), liver (6510-1), lung (6524-1)

• Data Normalization

version 5.0 software (Affymetrix, Santa Clara, CA) using default parameter settings. Scaling was not done via a MAS 5.0 Arrays were analyzed and expression values, called signal, was calculated for each gene by using Microarray Suit (MAS) option. Instead, the intensities of each array were log10 transformed and scaled to a constant reference value (global normalization). This reference value was the mean of all log intensities in all of the tissues.

Expression Profiles

Duplicate measurements were obtained for twelve normal human tissues hybridized against Affymetrix GeneChips HG-U95A-E. The intensity values (shown on the y-axis) were normalized and drawn on a novel scale, which is an intermediate between log and linear scales. This enables displaying several orders of magnitude on the same graph, while emphasizing the differences between them.

Aggregate Expression

The bar graphs represent the averaged expression level calculated for a given gene. The calculation is done by averaging all of the probe-sets individual profiles. The detailed expression profile with the annotation for each individual probesets are presented in the table on the given gene web-page.

Variation plots

intensity levels reach a threshold in at least one tissue. The variation of included and excluded probe-sets are visualized in the x-y plane: the x-axis shows Pearson's correlations between individual probe-sets vectors and the average tissue vector; the yaxis shows the relative length of an individual probe-set vector (its scalar length divided by that of the average vector). The Multiple probe-sets corresponding to the given gene are included for its tissue vector calculation only if their normalized average is shown as a black square, while individual probe-sets are depicted as colored circles.

Probe set annotation

(http://www.affymetrix.com/index.affx), wherein each probe-set on Affymetrix HG-U95 is constructed from 16 probes 25 The list of probes and their sequences was obtained from the Affymetrix public database

using the BLAT algorithm (Kent, W.J. (2002) BLAT--the BLAST-like alignment tool. Genome Res, 12, 656-64.) allowing one nucleotide long. 16 probes taken from each probe-set were aligned against the mRNA sequences from the most comprehensive the relationships of other genes that were aligned. Specificity and sensitivity parameters describe the quality of each probe-set. public databases using the GeneAnnot algorithm (http://genecards.weizmann.ac.il/geneannot/). The alignment was performed mismatch along the sequence. The quality scores of a probe-set are given per specific genes, while taking into consideration

Specificity calculation

specificity is calculated by the weighted summation of all probe values in the set, divided by the total number of aligned probes If a probe is aligned to a single gene its score will be 1. However, if it is aligned to n genes the value will be 1/n. The in the set.

Sensitivity calculation

Probe set sensitivity is calculated by the summation of the successfully aligned probes divided by the total number of probes in the set (e.g., 16).

Electronic Northern

Electronic Northern method

unique clones per gene per tissue. Clones are assigned to particular tissues by applying data-mining heuristics to Unigene's library information file *Hs.lib.info*. Electronic expression results were calculated by dividing the number of clones per gene by between log and linear scales. This enables displaying several orders of magnitude on the same graph, while emphasizing the the number of clones per tissue. They were then normalized by multiplying by 1M, and the obtained normalized counts are For the shown set of normal human tissues NCBI's Unigene dataset Hs. data is mined for information about the number of presented on the same root scale as the experimental tissue vectors. This scale (shown on the y-axis) is an intermediate differences between them.

Appendix C

Expression of *netrin-1*, *slit-1* and *slit-3* but not of *slit-2* after cerebellar and spinal cord lesions

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Keywords: axotomy, mouse, rat, robo, unc5h

Abstract

To determine whether members of the Netrin-1 and Slit families and their receptors are expressed after central nervous system (CNS) injury, we performed *in situ* hybridization for *netrin-1*, *slit-1*, 2 and 3, and their receptors (*dcc*, *unc5h-1*, 2 and 3, *robo-1*, 2 and 3) 8 days, 2–3 months and 12–18 months after traumatic lesions of rat cerebellum. The expression pattern of these molecules was unchanged in axotomized Purkinje cells, whereas *unc5h3* expression was upregulated in deafferented granule cells. Cells expressing *slit-2* or *dcc* were never detected at the lesion site. By contrast, cells expressing *netrin-1*, *slit-1* and *slit-3*, *unc5h-1*, 2 and 3, and *robo-1*, 2 and 3 (*rig-1*) could be detected at the cerebellar lesion site as soon as 8 days after injury. Expression of *unc5h-2*, *robo-1*, *robo-2*, *slit-1* and *slit-3* at the lesion site was maintained until 3 months, and up to 12–18 months for *unc5h-1* and 3 and *robo-3*. Likewise, in the mouse spinal cord, *netrin-1*, *slit-1* and *slit-3* were also expressed at the lesion site 8 days after injury. Most of the cells expressing these mRNAs were located at the centre of the lesions, suggesting that they are macrophages/activated microglial cells (macrophagic cells) or meningeal fibroblastic cells. The macrophagic nature of most Netrin-1-positive cells and the macrophagic or fibroblastic nature of Robo-1-positive cells were corroborated by double staining. Thus, Netrin-1, Slits and their receptors may contribute to the regenerative failure of axons in the adult CNS by inhibiting axon outgrowth or by participating in the formation of the CNS scar.

Introduction

In the mammalian central nervous system (CNS), adult neurons fail to regenerate their axons after lesion. It is known that this failure is partly due to the presence of axon growth-inhibitory molecules in the local environment of the severed axons in myelin (Filbin, 2003; Schwab, 2004) and in the glial scar (Moon et al., 2001). However, even after neutralization of these inhibitors, the number of severed axons that regenerate is low (Schwab et al., 1993), reflecting either the poor intrinsic ability of central neurons to regenerate and/or the existence of additional inhibitory factors.

One tempting hypothesis is that chemorepellent molecules, which collapse embryonic growth cones and repel developing axons and migrating neurons, could be upregulated at the lesion site and surrounding glial scar after adult CNS injury. Chemotropic molecules have been identified in three gene families, the Semaphorins, the Netrins and the Slits (Culotti & Kolodkin, 1996; Brose & Tessier-Lavigne, 2000). Several class 3 secreted Semaphorins are highly expressed after CNS lesions, suggesting that they could inhibit axonal regeneration (De Winter et al., 2002; Pasterkamp et al., 1998a, b, c, 1999; Pasterkamp & Verhaagen, 2001). In addition, expression of the transmembrane semaphorin, Sema 4D, is upregulated by oligodendrocytes after spinal cord lesions (Moreau-Fauvarque et al., 2003). By contrast, expression of the other members of these chemorepellent families has not yet been analysed

after traumatic lesion in mammalian CNS, the the most commonly used model for axon regeneration studies. Only an increase in *slit-2* mRNA in reactive astrocytes has been reported in the cryo-injured mouse cerebral cortex (Hagino *et al.*, 2003), a model not used to study axon regeneration.

The aim of this study was to determine whether netrin-1, slit-1, slit-2 and slit-3 and their receptors are expressed or upregulated after traumatic injury in the adult CNS of mammals. Netrin-1 has been shown to interact with the transmembrane receptors DCC (Deleted in Colorectal Cancer) and UNC5H (Keino-Masu et al., 1996; Ackerman et al., 1997; Leonardo et al., 1997; Forcet et al., 2002). In parallel, three members of the Roundabout (Robo) family, Robo-1 and 2 and Rig-1/Robo-3 have been shown to bind Slit molecules (Brose et al., 1999). It is known that glial cell reactivity depends on the species and on the site of the lesion. For instance, after a traumatic injury in the CNS, rats develop cavities whereas mice do not (Dusart & Schwab, 1994; Dusart & Sotelo, 1994; Steward et al., 1999; Morel et al., 2002). In mice, astrocytes enter the necrotic area of traumatic cerebellar injury, but they do not enter after traumatic spinal cord injury (Morel et al., 2002; Camand et al., 2004). Owing to these species and location differences, we decided to carry out first a complete longitudinal study (from 8 days to 18 months after a traumatic lesion) in the rat cerebellum. For that purpose, we analysed the expression of netrin-1, slit-1, slit-2 and slit-3 mRNAs and their receptors dcc, unc5h1, 2 and 3 and robo-1, 2 and 3. Thereafter, the results were compared with those obtained with netrin-1, slit-1, slit-2 and slit-3 mRNAs in the mouse spinal cord 8 days after the lesion, the period of maximal expression of chemotropic factors following cerebellar lesions.

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Materials and methods

All procedures were carried out in accordance with guidelines approved by the French Ministry of Agriculture, following European Standards. Twenty-one female Wistar rats (weighing 200 g at the time of lesion, Janvier, Le Genest St Isle, France), 12 female Swiss mice (weighing 20 g at the time of lesion, Janvier) and three slit-1 knockout (KO) mice (Plump et al., 2002) were used in this study. The rats were anesthetized with chloral hydrate (400 mg/kg i.p.) and the mice with ketamin (146 mg/kg) and xylazin (7.4 mg/kg). After the lesion, animals were returned to their cages and given free access to food and water. The procedures to induce cerebellar and spinal cord lesions were as described previously (Dusart & Sotelo, 1994; Camand et al., 2004).

Lesioned animals were divided into two groups, which were, respectively, prepared for immunohistochemistry (three rats for 8 days and 1 month and three mice with a survival time of 8 days) and in situ hybridization (three rats for each of 8 days, 2-3 months and 12-18 months, and three mice with a survival time of 8 days). For controls, 12 nonoperated animals were processed in the same way (three per procedure). The lesioned cerebella and spinal cords were sectioned in the parasagittal plane.

In situ hybridization

cDNA encoding rat slit-1, rat slit-2, rat slit-3, mouse netrin-1, rat dcc and rat Unc5h1, 2 and 3 were as described by Keino-Masu et al. (1996), Serafini et al. (1996), Leonardo et al. (1997) and Marillat et al. (2002). The in vitro transcription was carried out by using the Riboprobe Gemini System II buffers (Promega, Madison, WI, USA) and probes were labeled with ³⁵S UTP (1000 Ci/mm; Amersham, Arlington Heights, IL, USA) as described in Fontaine & Changeux (1989). In situ hybridization was performed on fresh frozen cerebellar and spinal cord sections as described in Wehrle et al. (2001). The autoradiographs were analysed via bright- and dark-field microscopy by using a Zeiss Axiophot microscope or a Leica DMR microscope. Some of the slices were counterstained with cresyl violet.

Immunohistochemistry

Rats and mice were anesthetized and perfused through the aorta with 0.12 M phosphate-buffered (pH 7.4) 4% paraformaldehyde. Brains or spinal cords were removed, postfixed for 4 h and cryoprotected in 30% sucrose for 2 days. The cerebella and the spinal cord were cut in the parasagittal plane (24-µm-thick free-floating sections) on a freezing microtome (Leica). Rabbit polyclonal antibody against Netrin-1 (PC364, diluted 1:20, Oncogen research Products, Cambridge, UK; Madison et al., 2000) and goat polyclonal antibody against Robo-1 (diluted 1: 250, R&D Systems Europe, Lille France) were used. Rabbit polyclonal antibodies against fibronectin (diluted 1:500, Sigma, St Louis, MO, USA) were applied to reveal the presence of meningeal fibroblasts and non-CNS elements. Isolectin B4 from Bandeira simplicifolia coupled to FITC (diluted 0.02 mg/mL; Sigma) was used to visualize microglial cells and macrophages (Streit & Kreutzberg, 1987). The sections were incubated for 1 h in PBS containing 0.25% Triton X-100 (Sigma), 0.2% gelatin (Prolabo, Fontenay-sous-Bois, France) and 0.1% sodium azide (PBSGTA) containing 0.1 M lysine (blocking solution). Then, the sections were incubated overnight at room temperature in the primary antibodies at the dilutions indicated above in PBSGTA. The rabbit polyclonal antibodies against Netrin-1 and fibronectin were visualized with goat

antirabbit antibodies coupled to Cy3 (diluted 1:200, Jackson-Immunoresearch, West Grove, PA, USA) and donkey antigoat coupled to AMCA (diluted 1:50, Jackson Immunoresearch), respectively. The mouse monoclonal antibody against Robo-1 was revealed with donkey antigoat coupled to Cy3 (diluted 1: 200, Jackson Immunoresearch). Some of the sections were counterstained with Hoechst (bisbenzimide, 1: 1000, Sigma) to label cell nuclei. Finally, the slices were washed several times with PBS, and mounted in mowiol (Calbiochem, La Jolla, CA, USA).

The sections were analysed using a Leica DMR microscope equipped with a coolsnap-fx camera (Princeton Instruments, Evry, France). Images were captured on a Dell computer using Metaview software (Universal Imaging Corporation, West Chester, PA, USA). In some cases, double staining was confirmed on 1-µm-thick confocal sections observed with a Leica confocal microscope (Plateforme d'Imagerie, IFR83). Images were treated and assembled using Adobe Photoshop software version 6.0 (Adobe System, Inc.).

Results

Expression in the cerebellum

In parasagittal sections of rat cerebellum 8 days after lesion, the knife cut only affects the vermis and is easily identified as the narrow gap dividing the lobules into dorsal and ventral portions (Fig. 1A). Under the cut, particularly in the ventral portions, large necrotic areas (Fig. 1A) filled with macrophages and activated microglial cells are generated (Fig. 1B). The narrow gap and these necrotic areas are considered to be the center of the lesion. They are surrounded by a wider zone of reactive astrocytes considered as the periphery of the lesion (Fig. 1C). This area extends throughout the white matter and most of the grey matter of lobules IV and VII, and contains not only reactive astrocytes but also microglial cells, oligodendrocytes and granule cells (Dusart & Sotelo, 1994; Dusart et al., 1999). Two months after the lesion, the center of the lesion is either a cavity or a thin line containing macrophages and activated microglial cells (Fig. 1D and F). These central areas are surrounded by highly activated astrocytes that delineate the glial scar (Fig. 1E and G).

Netrin-1

In the intact adult rat cerebellum, netrin-1 mRNA is exclusively expressed in interneurons of the molecular layer, Purkinje cells and deep nuclear neurons, as previously described in younger animals (Livesey & Hunt, 1997; Alcantara et al., 2000). Eight days after the lesion, this neuronal expression remains unchanged. By contrast, at the center of the lesion, new cells organized in clusters strongly express netrin-1 (see Fig. 6A, Table 1), whereas only sparse cells are labeled at the periphery in the glial scar. Two months postlesion, no netrin-1 expression can be detected at the center of the lesion (Table 1). From this time point onwards, netrin-1 expression is similar to that observed in the intact cerebellum.

Whatever the time after injury, expression of dcc was similar to that in the intact cerebellum (i.e. faint labeling of the Purkinie cells), as previously described (Bloch-Gallego et al., 1999; Table 1).

Unc5h-1, 2, 3

In the intact cerebellum, the neurons expressing unc5h1 are deep nuclear neurons and granule cells (Fig. 2A). Unc5h2 is detected in granule cells, molecular layer interneurons and glial cells in the white

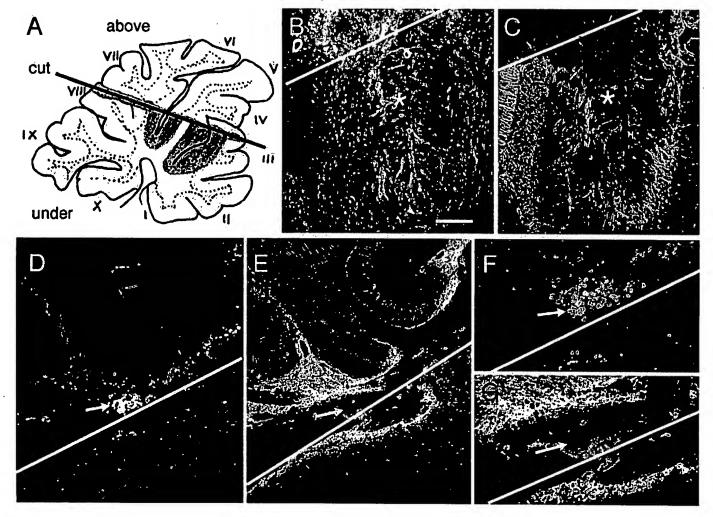


FIG. 1. (A) Schematic representation of a parasagittal section of a lesioned cerebellum. The cut (dark line) delineates the sectioned lobules (IV, V, VI and VII) located above the cut from the nonlesioned lobules (I, II, III, VIII, IX and X) located beneath the cut. The grey areas represent what we term here the lesion center. Asterisks indicate the necrotic areas under the cut. Adapted from Dusart & Sotelo (1994). Parasagittal cerebellar sections at 8 days post lesion (B and C), and 2 months post lesion (D-G) double stained with Isolectin B4 (B, D and F) and anti-glial fibrillary acidic protein (GFAP) (C, E and G). Note the absence of GFAP immunostaining and the presence of Isolectin B4-positive cells in the center of the lesion (asterisk indicates as in A the necrotic area). The white lines represent the cuts. Arrows in D-G point to the same area. Scale bar in B, 240 µm (B-D) and 120 µm (E and F).

matter (Fig. 2B). Purkinje cells, some cells in the granule cell layer that are presumably Golgi cells, and granule cells in lobule X express unc5h3 (Fig. 2C). In the transected cerebella, additional cells express unc5h1, 2 and 3 at the center of the lesion at 8 days (Fig. 2D). Unc5h2 expression in these cells is maintained up to 2 months (Fig. 2E), whereas expression of unc5h1 and 3 is maintained up to 12 months (Fig. 2F, Table 1). At any time after the lesion, unc5h3 expression can be detected at the center of the lesion and in the granule cells located in the lobules dorsal to the lesion cuts (Fig. 2F).

Slit-1, 2, 3

In the cerebellum, as described previously (Marillat et al., 2002), slit-1, 2 and 3 are expressed in neurons of the lateral nucleus, slit-1 and 2 in the interpositus nucleus, slit-2 in Purkinje cells of lobules IX and X, and slit-3 in granule cells. There was no modification of these expression patterns after the lesion (Fig. 3). However, many cells located at the center of the lesion strongly express slit-1 mRNA at 8 days (Fig. 3A) and 2 months (Fig. 3B) but not after 3 months (Table 1). A few cells, at the lesion center, also express slit-3 mRNA up to 2 months postlesion (Fig. 3C and D). This additional expression was not detected for slit-2 transcripts (Table 1).

Robo-1, 2 and 3

In the intact cerebellum, robo-1 can be detected in Purkinje cells, deep nuclear neurons and fibroblastic cells (Fig. 4A; Marillat et al., 2002). Robo-2 is expressed in deep nuclear neurons, Purkinje cells and a subpopulation of granule cells located around the fissura prima (Fig. 4B); and finally, robo-3/rig-1 transcripts are present in granule cells, molecular layer interneurons and deep nuclear neurons (Fig. 4C). Following lesions, many cells strongly express robo-1, 2 and 3 at the center of the lesion (Fig. 4D-F). Expression is maintained up to 2 and 3 months for robo-1 and 2 (Fig. 4E), and up to 12-18 months for robo-3 (Fig. 4F).

Expression in the spinal cord

In the intact adult mouse spinal cord, cells expressing *netrin-1* mRNA are scattered within the grey and the white matter, and may correspond to motoneurons, and multiple classes of interneurons and oligodend-rocytes, respectively (Manitt *et al.*, 2001). As previously reported (Moreau-Fauvarque *et al.*, 2003; Camand *et al.*, 2004), 8 days after a dorsal hemisection of the mouse spinal cord, two lesion areas can be distinguished: the center of the lesion filled with fibroblastic cells,

TABLE 1. Presence of guidance cues at the center of the cerebellar lesion

Molecule	8 days	2-3 months	12-18 months	
netrine-1	+	_	-	
dcc	_	_	_	
unc5h1	+	+	+	
unc5h2 .	+	+	_	
unc5h3	+	+	+	
slit-1	+	+	_	
slit-2	_	_	_	
slit-3	+	+ '	_	
robo-1	+	+	_	
robo-2	+	+	_	
robo-3/rig-1	+	+	+	

macrophages and activated microglial cells, and the periphery of the lesion defined by the presence of activated astrocytes, activated microglial cells, oligodendrocytes and polydendrocytes. In addition to the cells encountered in the intact spinal cord, numerous cells with strong netrin-1 mRNA expression are detected at the center of the lesion (Fig. 5A).

In the intact mouse spinal cord, slit-1, slit-2 and slit-3 mRNAs are detected in all lamina of the thoracic grey matter but with slightly different repartitions. Slit-1 expression is much stronger in the dorsal than in the ventral spinal cord (Fig. 5B). Expression of slit-2 is similar to that of to slit-1, with the highest level in the ventral region (Fig. 5C) mainly in large cells, probably motoneurons (Fig. 6B and C). Expression of slit-3 is similar to that of slit-2, but is slightly less

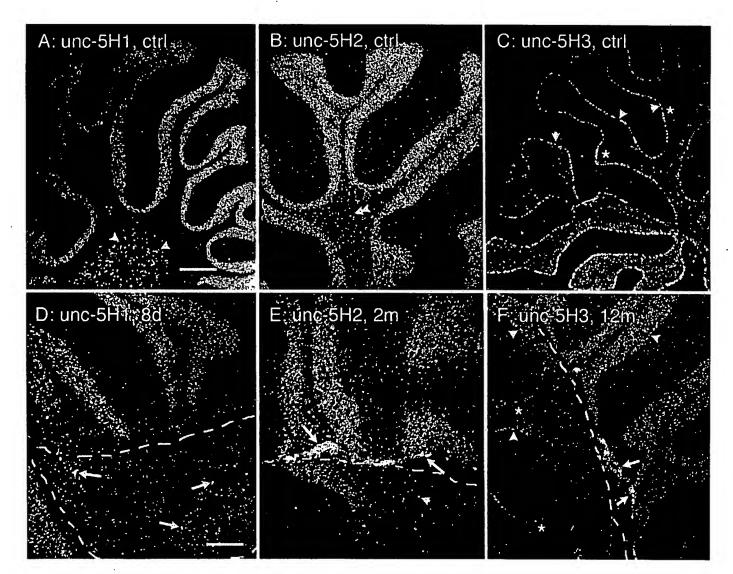


FIG. 2. Expression of unc5h in cerebellum. Parasagittal cerebellar sections of control (ctrl, A, B and C), 8 days post lesion (8d, D), 2 months post lesion (2m, E) and 12 months post lesion (12m, F) hybridized with the unc5h1 (unc-5H1, A and D), unc5h2 (unc-5H2, B and E) and unc5h3 (unc-5H3, C, F) antisense probes. (A) Note the presence of unc-5h1-labeled granule cells (black asterisk) and deep nuclear neurons (arrowheads). (B) Note the presence of unc-5h2-labeled granule cells (black asterisk), and glial cells in the white matter (double arrowhead). (C) Note the presence of unc-5h3-labeled Purkinje cells (arrowheads) and that the only labeled granule cells are present in lobules X and IX (black asterisk), whereas granule cells in the other lobules are not labeled (white asterisks). (D) Eight days after lesion (8d), the granule cell neurons are still labeled (black asterisk) and numerous labeled cells (arrows) can be observed at the lesion site (dotted line). (E) Two months after the lesion (2m), in addition to the labeled granule cells (black asterisk), molecular interneurons and glial cells in the white matter (arrowheads), numerous clustered cells are also labeled (arrows) around the cut (dotted line). (F) Note the presence of unc-5h3-labeled cells (arrows) around the cut (dotted line) 12 months after the lesion (12m). Interestingly, the granule cells that are located in the sectioned lobules (above the cut) are now labeled (black asterisks), whereas the granule cells in the other lobules are still not labeled (white asterisks). Purkinje cells are still labeled (arrowheads). Scale bar in A, 670 µm (A and C), 330 μm (B, D and F) and 250 μm (E).

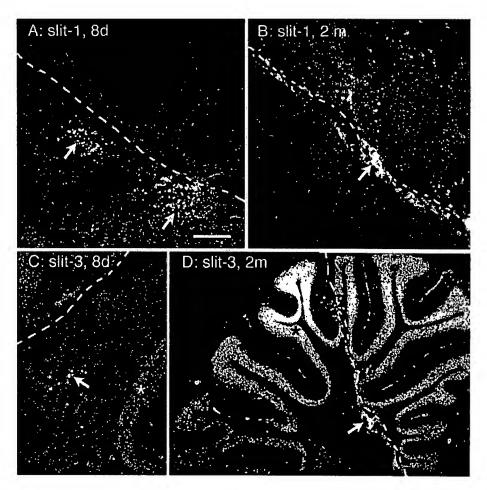


Fig. 3. Expression of slit-1 and slit-3 in the lesioned cerebellum. Parasagittal sections of lesioned cerebellum (8 days A and C, 2 months B and D) hybridized with the slit-1 (slit-1, A and B) and the slit-3 (slit-3, C and D) antisense probes. (A) Note the presence of two clusters of numerous heavily labeled cells (arrows) under the knife cut (dotted line). These areas are similar to those represented in Fig. 1A by asterisks. (B) Note the presence of numerous heavily labeled cells (arrow) around the knife cut (dotted line). (C) Note the presence of numerous heavily labeled cells (arrow) under the cut (dotted line). The granule cell layer is labeled (white asterisk). (D) Note the presence of numerous heavily labeled cells (arrow) around the knife cut (dotted line). The granule cell layer is labeled (black asterisk). Scale bar in A, 330 μm (A-C) and 670 μm (D).

intense (Fig. 5D). The cresyl violet counterstaining suggests that the cells expressing *slit* mRNAs are neurons and not glial cells, given that they are large and weakly stained by cresyl violet (Fig. 6C).

Eight days after a mouse spinal cord dorsal hemisection, slit-1 and slit-3 mRNAs are detected in cells at the center of the lesion (Fig. 5E and F). Here again, as in the cerebellum, expression of slit-2 was not observed (data not shown). At the center of the lesion, slit-3 mRNA seems more strongly expressed than that of slit-1 (compare Fig. 5F with Fig. 5E), whereas in the cerebellum there are more cells expressing slit-1 than slit-3 (see above, Fig. 3A and C). We were able to validate our results by performing slit-1 in situ hybridization in a slit-1 KO mouse with a spinal cord lesion. Indeed, in this case, no slit-1 mRNA was detected even at the center of the lesion (Fig. 5G). Moreover, in the slit-1 KO mouse, slit-2 mRNA was not upregulated (Fig. 5H).

Characterization of the cells

Our in situ hybridization results in cerebellar and spinal cord lesions have revealed cells strongly expressing netrin-1 mRNA in and around the lesion, following a distribution pattern that mimics that of macrophagic and fibroblastic cells (see above). To characterize these cells further, we performed double labeling experiments using an

antibody against Netrin-1 and the Isolectin B4 coupled to FITC. On sections from intact animals, Netrin-1 immunostaining, although faint, corresponds to the labeling observed with *in situ* hybridization: molecular interneurons and Purkinje cells in the cerebellar cortex, some neurons in the grey matter and small cells in the white matter of the spinal cord (data not shown). In both types of lesions, clusters of round Netrin-1-immunoreactive cells are present at the lesion center (Fig. 6D–G). In addition, a mixture of round and ramified cells are observed at the periphery of spinal cord lesions (Fig. 6H–J) and to a lesser extent at the periphery of the cerebellar lesions (data not shown). However, although almost all Netrin-1-immunoreactive cells are double stained with Isolectin B4, only a small fraction of the Isolectin B4-positive cells are Netrin-1 immunoreactive (Fig. 6D–G). Thus, Netrin-1-positive cells belong to a subpopulation of activated microglial cells and macrophages.

In the intact cerebellum, Robo-1 is coexpressed in blood vessels with fibronectin (Fig. 6K, M and N) but not with Isolectin B4 (Fig. 6K, L and N). At the lesion site, in addition to these vascular associated Robo-1-expressing cells, which maintain their fibronectin expression (data not shown), there are other Robo-1-expressing cells that are double stained with Isolectin B4 (Fig. 6O and P). Therefore, as reported above for Netrin-1, only a subpopulation of Isolectin B4-positive cells are Robo-1 immunoreactive (Fig. 6O and P). For

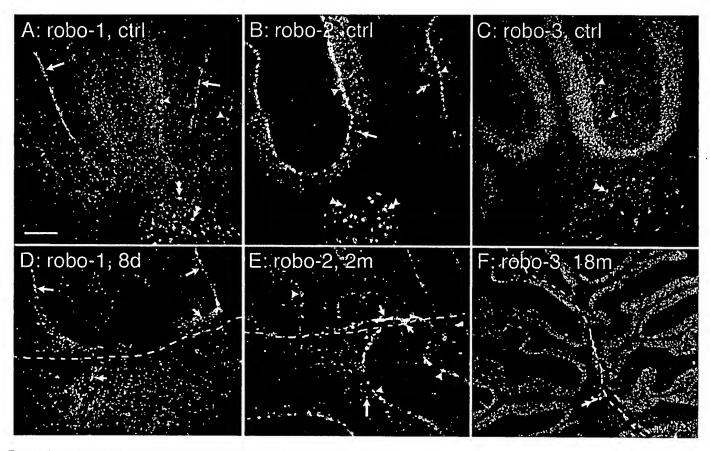


FIG. 4. Expression of robos in the cerebellum. Parasagittal cerebellar sections of control (A-C), 8 days post lesion (D), 2 months post lesion (E) and 18 months post lesion (F) hybridized with the robo-1 (robo-1, A and D), robo-2 (robo-2, B and E) and robo-3/rig-1 (robo-3, C and F) antisense probes. (A) Note the presence of strong robo-1 labeling in the meninges (arrows) and in the deep nuclear neurons (double arrowheads) and of a weak expression in the Purkinje cells (arrowheads). (B) Note the presence of a strong expression of robo-2 in Purkinje cells (arrowheads), some presumably Golgi cells (arrows) and deep nuclear neurons (double arrowheads). The granule cell layer of some lobules is labeled (black asterisk), but not in other lobules (white asterisks). (C) Note the presence of robo-3-labeled granule cells (black asterisk), molecular interneurons (arrowheads) and deep nuclear neurons (double arrowheads). (D) Note the presence of numerous heavily robo-1-labeled cells (short arrows) in the continuation of the meninges (long arrows) and under the cut (dotted line). (E) Two months after lesion, numerous heavily robo-2-labeled cells (short arrows) can be detected around the cut (dotted line). Note the presence of a strong expression of robo-2 in Purkinje cells (arrowheads) and in some presumably Golgi cells (arrows). (F) Up to 18 months after the lesion, some heavily robo-3-labeled cells (short arrow) can be detected around the cut (dotted line). The white asterisk indicates the labeled granule cells. Scale bar in A, 240 µm (A-E) and 670 µm (F).

identification of cells labeled with the other probes and in the absence of specific antibodies, we carried out an analysis on adjacent sections. These were double labeled with Hoechst stain to delineate the different cerebellar layers and with Isolectin B4 (Fig. 6Q), fibronectin (Fig. 6Q) or robo-1 (Fig. 6R), slit-1 (Fig. 6S), slit-3 (Fig. 6T), rig-1 (Fig. 6U), dcc (Fig. 6V), and unc5h1, 2 and 3 probes (data not shown). As described previously, no cells expressing dcc were detected at the lesion site (Fig. 6V). By contrast, the other mRNA probes always labeled the same cell clusters located at the lesion center (Fig. 6R-U) and containing Isolectin B4-positive cells as well as fibronectinpositive cells (Fig. 6Q). These results suggest that the cells revealed with slit-1, slit-3, rig-1, and unc5h1, 2 and 3 in situ hybridization are macrophagic or fibroblastic cells. Therefore, the population of macrophages and fibroblastic cells, at the lesion center, seems to be heterogeneous, and composed of several subclasses of specialized cells expressing different chemotropic factors.

Discussion

The aim of this work was to study the expression of chemotropic factors and their receptors following traumatic lesions in the adult rat cerebellum and mouse spinal cord. Expression patterns of these ligands

and receptors were first analysed by in situ hybridization in control adult animals. We corroborated the neuronal expressions of netrin-1, dcc, unc5h3, slits and robos in rat cerebellum, and added new information on the expressions of unc5h1 and 2 in the cerebellum and of slits in the mouse spinal cord. Following lesion, the neuronal expression pattern of most of these molecules remained unchanged, although unc5h3 expression was upregulated in de-afferentiated granule cells. More importantly, cells expressing netrin-1, unch5h1. 2 and 3, slit-1 and 3, and robo-1, 2 and 3 were systematically present at the lesion site (lesion center and close periphery). Their position and the double staining with Isolectin B4 or with anti-fibronectin antibodies suggested that these cells were macrophagic and/or fibroblastic cells. The present results suggest that chemotropic molecules may contribute to inhibition of axon regeneration and glial scar formation.

Neuronal expressions of netrin-1, slits and their receptors. except that of unc5h3, are unchanged after traumatic lesions

The expression of chemotropic molecules in the developing CNS has been well documented (Ackerman et al., 1997; Leonardo et al., 1997; Livesey & Hunt, 1997; Bloch-Gallego et al., 1999; Alcantara et al., 2000; Marillat et al., 2002) but much less is known regarding their

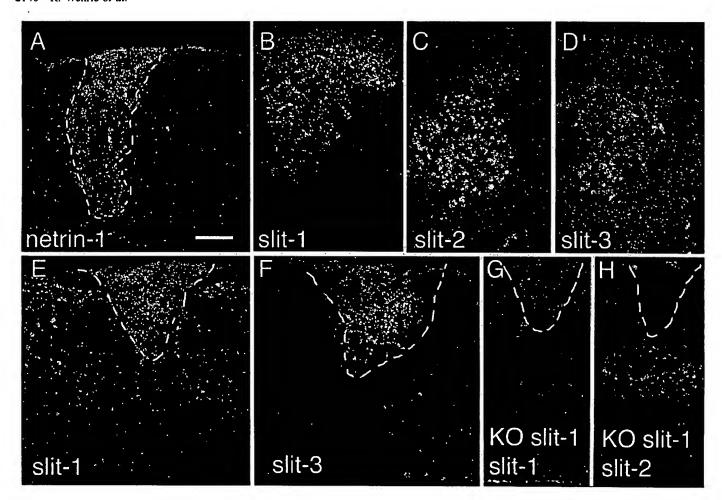


FIG. 5. Expression of netrin-1 and slit mRNAs in the spinal cord. (A) Parasagittal section of sectioned spinal cord, 8 days post lesion, hybridized with the netrin-1 (netrin-1) antisense probe. Note the presence of labeled cells in and around the lesion (dotted line). (B-D) Coronal sections of control spinal cord hybridized with the slit-1 (B), slit-2 (C) and slit-3 (D) antisense probe, illustrating the pattern of expression of the three slit mRNAs. (E and F) Parasagittal sections of sectioned spinal cord, 8 days post lesion, hybridized with the slit-1 (E) and slit-3 (F) antisense probe. Note the presence of labeled cells within the lesion site (dotted line). The density of the autoradiographic signal is somewhat higher with the slit-3 than with the slit-1 antisense probe at the lesion center. (G and H) Parasagittal sections of KO slit-1 sectioned spinal cord, 8 days post lesion, hybridized with the slit-1 (G) and slit-2 (H) antisense probes. Note the total absence of labeled cells in the spinal cord in G and only within the lesion site (dotted line) in H. Scale bar in A, 250 µm (A) and 350 µm (B-H).

expression in the adult (Manitt et al., 2001; Marillat et al., 2002). Our work showed that unc5h1 and 2 are expressed in granule cells and unc5h1 in deep nuclear neurons, whereas unc5h2 is expressed in molecular layer interneurons and glial cells in the white matter. In the adult cerebellum, the expression patterns of slits and of robos are similar to those described by Marillat et al. (2002). In the spinal cord, we show here that the three slits are most probably expressed with different intensities in neurons. In addition, slit-1-expressing cells are detected more predominantly in the dorsal part of the spinal cord, whereas slit-2 and slit-3 are more highly expressed ventrally, including presumed motoneurons.

Changes in neuronal expression of chemotropic molecules (with the exception of unc5h3, see below) were not detected after lateromedial transection of the cerebellum or dorsal hemisection of the spinal cord. In particular, Purkinje cells do not regulate expression of netrin-1 or slits after axotomy, contrary to what has been reported for other chemotropic molecules and for other neurons such as olfactory neurons (Pasterkamp et al., 1998b; Williams-Hogarth et al., 2000; Astic et al., 2002) and retinal ganglion cells (Petrausch et al., 2000; Ellezam et al., 2001). This difference in the postaxotomy reaction observed for Purkinje cells (no increase of netrin-1 or of slit mRNAs) confirms the diversity of the neuronal responses following axotomy.

Postlesion modifications of the receptors for chemotropic molecules have been reported: dcc, unc5h1 and unc5h2 are rapidly downregulated after axotomy of retinal ganglion cells (Petrausch et al., 2000; Ellezam et al., 2001). After cerebellar lesion, we did not detect any changes in the neuronal expression of dcc, unc5h1 and 2, robo-1 and 2, or rig-1. However, unc5h3 expression was upregulated in the granule cells above the lesion site, i.e. in the sectioned lobules. These granule cells were not axotomized by the lesion, but a large proportion of them was deafferentiated. Indeed, transection of the cerebellar white matter axotomized not only Purkinje cells but also climbing and mossy fibers, the latter being the extracerebellar afferent fibers of the granule cells. Interestingly, unc5h3 is transiently expressed by granule cells during development (Ackerman et al., 1997), suggesting that after lesion granule cells reinitiate a developmental program.

Netrin-1, unc5hs, slits and robos are expressed by a subpopulation of macrophagic and/or fibroblastic cells

In contrast to the almost complete lack of changes in their neuronal expressions, netrin-1, slit-1 and 3, robo-1 and 2, rig-1, and unc5h-1, 2 and 3 transcripts appeared at the lesion center. The position of these

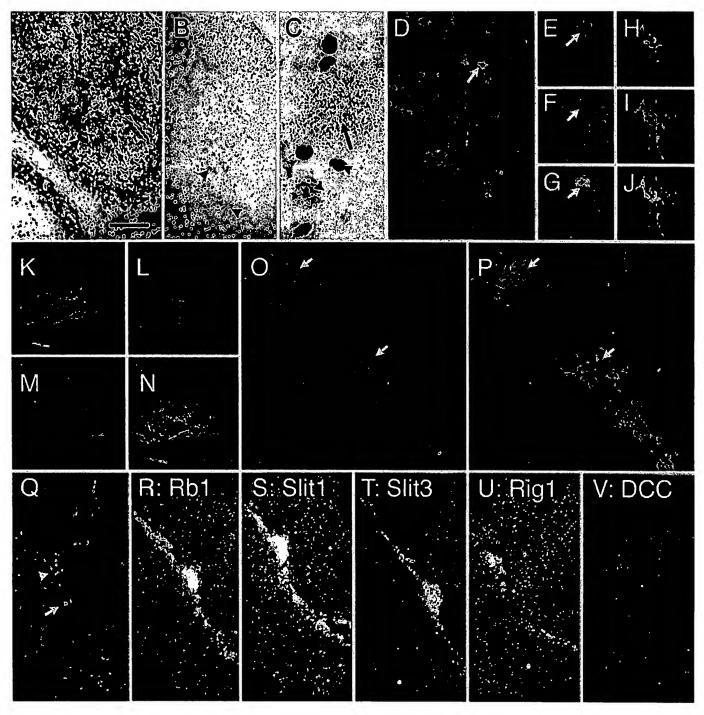


FIG. 6. (A) Parasagittal section of lesioned cerebellum, 8 days post lesion, hybridized with the netrin-1 antisense probe and counterstained with cresyl violet (CV), illustrating numerous heavily labeled cells (arrow) in a region ventral to the cut, containing a large cell infiltrate, corresponding to the presumptive necrotic area (delineated by a dotted line; area similar to those indicated by asterisks in Fig. 1A). (B) Coronal section of control spinal cord hybridized with the slit-2 antisense probe and conterstained with CV. Arrowheads point to labeled cells. Low magnification for orientation purposes, (C) Coronal section of control spinal cord hybridized with the slit-2 antisense probe and counterstained with CV. Note that a large, faintly CV-stained cell highly expresses slit-2 (arrow), a small, faintly CVstained cell expresses also slit-2 (arrowhead) in the ventral horn whereas the small, intensely CV-stained cells (double arrowhead) do not express slit-2. (D-J) Double staining, with anti-Netrin-1 in red (D, E, G, H and J) and Isolectin B4 in green (D, F, G, I and J), of macrophagic cells at the center of a cerebellar lesion (D-G) and of microglial cells at the periphery of a spinal cord lesion (H-J) 8 days post lesion. Arrows in D-G point to the same cell. (K-N) Confocal photomicrographs of a cerebellar parasagittal slice 2 months after lesion triple labeled with anti-Robo-1 (red, K and N), Isolectin B4 (green, L and N) and anti-fibronectin (blue, M and N). Note that Robo-1 and fibronectin stainings colocalize (presence of violet in N) whereas Robo-1 and Isolectin B4 stainings do not colocalize (absence of yellow in N). (O and P) Photomicrographs of a cerebellar sagittal slice 2 months after lesion triple labeled with anti-Robo-1 (red, O and P), Isolectin B4 (green, P) and antifibronectin (blue, O and P). Note that cells expressing Robo-1 are also stained with Isolectin B4 (O and P, arrows). (Q-V) Photomicrographs of adjacent sections from a 2-month-old cerebellar lesion stained with (Q) Hoechst (blue), Isolectin B4 (green) and anti-fibronectin (red); (R) robo-1 antisense probe; (S) slit-I antisense probe; (T) slit-3 antisens probe; (U) rig-I antisense probe; (V) dcc antisense probe. Note that in all the photomicrographs with exception of V, cells expressing the different mRNAs are present in the same area as those stained with Isolectin B4 (arrowheads in Q) or fibronectin (arrow in Q). Scale bars, 85 µm (A), 300 μm (B), 20 μm (C), 50 μm (D and K-N), 25 μm (E-J and O-P) and 250 μm (Q-V).

newly expressing cells at the center of the lesion suggests that they are not neural cells because neurons, oligodendrocytes and astrocytes were never found at such location. Indeed, our previous work has shown that there are many macrophages or activated microglial cells, as well as endothelial cells and fibroblasts, at the lesion center (Dusart & Sotelo, 1994; Camand et al., 2004).

With regard to astrocytes, our results differ from those recently reported in reactive astrocytes after a cerebral cortical cryolesion, where *slit-2* mRNA expression was described (Hagino *et al.*, 2003). In our two post-traumatic central structures, *slit-2* mRNA was not detected in or around the lesion, and *slit* mRNAs were not detected in astrocytes, suggesting that this discrepancy is probably due to the type of lesion (cryolesion vs. traumatic injury) rather than to its location.

Furthermore, the macrophagic and/or fibroblastic nature of the cells newly expressing chemotropic factors or their receptors is supported by the data reported in this study. In short-term lesions (8 days) these cells were located in the large necrotic region, and were double labeled with anti-Netrin-1 antibodies and Isolectin B4, indicating that they belong to macrophages or activated microglial cells. Similarly, many cells populating the necrotic region and stained with Isolectin B4 or anti-fibronectin antibodies were double labeled with anti-Robo-1 antibodies or, on adjacent sections, labeled for different chemotropic molecules or their receptor mRNAs, suggesting that most of the cells expressing chemotropic factors at the lesion site are macrophagic or fibroblastic cells.

In conclusion, netrin-1 is expressed by a subpopulation of macrophages and ramified microglial cells. Similarly, slit-1 and 3 and the receptors unc5h1, 2 and 3 and robo-1, 2 and 3 are also be expressed – at least partly – by macrophagic cells, and probably also by fibroblasts, as already demonstrated for Sema-3A (Pasterkamp et al., 1999; Pasterkamp & Verhaagen, 2001). These results suggest that within the scar, different cell types are able to secrete different chemorepellent molecules according to the lesion type.

Potential roles of these molecules in axon regeneration and glial scar formation

It is generally accepted that the failure of axonal regeneration in the mammalian CNS is the combined result of intrinsic neuronal properties and of environmental factors in the vicinity of sectioned axons. Since the classical work of Schwab et al. (1993), it has been shown that the adult CNS contains inhibitory molecules preventing axon growth and regeneration. Membrane neurite outgrowth inhibitors have been identified on oligodendrocytes and myelin: Nogo-A, an antigen of the IN-1 antibody (Chen et al., 2000; GrandPre et al., 2000), myelin-associated glycoprotein (McKerracher et al., 1994; Mukhopadhyay et al., 1994), Tenascin-R (Pesheva & Probstmeier, 2000), myelin-oligodendrocyte glycoprotein (Wang et al., 2002) and recently Sema-4D (Moreau-Fauvarque et al., 2003). Chondroitin sulfate proteoglycans have been demonstrated to be major inhibitory molecules of the glial scar (Moon et al., 2001). Furthermore, all secreted class 3 Semaphorins have been detected in the scar after different types of lesions (Pasterkamp et al., 1998b, c; Pasterkamp & Verhaagen, 2001; De Winter et al., 2002). Here we report that, in addition to these inhibitory molecules, a subpopulation of macrophages and activated microglial cells, and probably meningeal cells, express and thus might secrete chemotropic molecules such as Netrin-1, Slit-1 and Slit-3 with a preponderant location at the lesion center. Neuronal expression of the chemotropic receptors is maintained after the lesion and some of them are expressed in Purkinje cells. Thus,

these chemotropic molecules could play a role in the failure of axon regeneration. However, because the number of macrophages expressing chemotropic factors is low and spatially restricted 2 months after the lesion, it is unlikely that these molecules could play a major role in the long-term failure of central axon regeneration.

It is well established that axon guidance molecules are also involved in cell migration. For instance, Netrin-1 and Slits influence the tangential migration of several types of neurons (Bloch-Gallego et al., 1999; Yee et al., 1999; Zhu et al., 1999; Alcantara et al., 2000; Causeret et al., 2002; Marin et al., 2003; Marillat et al., 2004; Nguyen-Ba-Charvet et al., 2004). Slits inhibit leucocyte migration (Wu et al., 2001) and vascular endothelial cell migration (Wang et al., 2003). Likewise, Netrin-1 modulates endothelial cell migration through Unc5h2 (Lu et al., 2004; Park et al., 2004). Thus, it is possible that expression of Netrin-1 and Slits in macrophagic cells at the lesion center is related to control of their migration to the necrotic region and to the neoangiogenesis that occurs after the CNS lesions. Last, DCC and Unc5h belong to a family of 'dependence receptors'. so called because they induce apoptosis when unbound to their ligand (Mehlen et al., 1998; Llambi et al., 2001; Mehlen & Mazelin, 2003; Thiebault et al., 2003). Thus, it is possible that the balance between expression of netrin-1 and unc5h regulates the survival of macrophages. Interestingly, Netrin-1 is expressed only during the first 8 days and disappears thereafter in parallel with the decrease in the number of macrophages. The migration of macrophages, their subsequent elimination and the revascularization of the lesioned CNS are related to the process of scar formation, which is essential in determining the outcome of axon regeneration.

We have shown here that the expression of chemotropic factors following traumatic lesion is different in rat cerebellum and in mice spinal cord. For example, *slit-1* is more highly expressed in the cerebellum and *slit-3* in the spinal cord. More importantly, cells newly expressing chemotropic molecules after lesion are found in clusters in the cerebellum whereas they are more uniformly distributed in the spinal cord. It is of note that the scarring process, which involves both activation and migration of glial cells, is also different between rat and mice (Dusart & Schwab, 1994; Dusart & Sotelo, 1994; Steward *et al.*, 1999; Morel *et al.*, 2002; Camand *et al.*, 2004). Thus, we propose that the differences in expression of the Slit molecules at the lesion site between rat cerebellum and mouse spinal cord partly reflect the differences observed in the scarring processes in these two different central regions and species.

Acknowledgements

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Abbreviations

CNS, central nervous system; DCC, Deleted in Colorectal Cancer; GFAP, glial fibrillary acidic protein; KO, knock-out; Robo, Roundabout.

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Appendix D

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robo Antibody / robo Antibodies

PRODUCT NAME	CATALOG #	ISOTYPE	EPITOPE	APPLICATIONS
robo1 (N-20) Antibody	sc-16611	goat IgG	N-terminus (h)	WB, IF
robo1 (I-20) Antibody	sc-16612	goat IgG	N-terminus (h)	WB, IP, IF
robo1 (H-200) Antibody	sc-25672	rabbit IgG	1452-1651 (h)	WB, IP, IF
Robo1 (dN-19) Antibody	sc-19715	goat IgG	internal (Dm)	WB, IF
Robo1 (dP-20) Antibody	sc-19716	goat IgG	internal (Dm)	WB, IF
robo2 (C-20) Antibody	sc-16615	goat IgG	internal (h)	WB, IF
robo2 (H-100) Antibody	sc-25673	rabbit IgG	1281-1380 (h)	WB, IP, IF
robo2 (D-16) Antibody	sc-31605	goat IgG	Internal (h)	WB, IF
robo2 (G-20) Antibody	sc-31606	goat IgG	internal (h)	WB, IF
robo2 (K-18) Antibody	sc-31607	goat IgG	C-terminus (h)	WB, IP, IF
Robo2 (dN-20) Antibody	sc-19718	goat IgG	N-terminus (Dm)	WB, IF
Robo2 (dC-20) Antibody	sc-19720	goat IgG	C-terminus (Dm)	WB, IF
robo3 (C-14) Antibody	sc-46493	goat IgG	C-terminal (h)	WB, IF
robo3 (N-17) Antibody	sc-46495	goat IgG	N-terminal (h)	WB, IF
robo3 (C-18) Antibody	sc-46496	goat IgG	C-terminal (h)	WB, IF
Robo3 (dN-20) Antibody	sc-19721	goat IgG	N-terminus (Dm)	WB, IP, IF
robo4 (C-20) Antibody	sc-46497	goat IgG	C-terminus (h)	WB, IP, IF
robo4 (D-19) Antibody	sc-46498	goat IgG	internal (h)	WB, IF
robo4 (N-17) Antibody	sc-46499	goat IgG	N-terminus (h)	WB, IF
robo4 (S-16) Antibody	sc-46500	goat IgG	internal (h)	WB, IF

robo Antibody / robo specific siRNA gene silencers are also available. These include: robo1 siRNA (h): sc-42252, robo2 siRNA (h): sc-42254, robo2 siRNA (m): sc-42255, robo3 siRNA (h): sc-44498, robo3 siRNA (m): sc-444499, and robo4 siRNA (m): sc-44501.



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